



```

Db      61 CAASGTFDDYGSWROAPGKLEWVSGINMNGSGTGYADSVKGRVTTISRDAKNSLYL 120
QY      121 QNMSLRAEDTAVYYCAKIIAGAGRWYFDLMGKGTVTYVSSGGSGGGSGGSSSELTQ 180
Db      121 QNMSLRAEDTAVYYCAKIIAGAGRWYFDLMGKGTVTYVSSGGSGGGSGGSSSELTQ 180
QY      181 DPAVSVALCQTVRITCQGSLSRSYASWYQOKPGAPVLYTGKNNRPSGIDPRFSGSSS 240
Db      181 DPAVSVALCQTVRITCQGSLSRSYASWYQOKPGAPVLYTGKNNRPSGIDPRFSGSSS 240
QY      241 GNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAEQKLI 300
Db      241 GNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAEQKLI 300
QY      301 SEEDLINGAA 309
Db      301 SEEDLINGAA 309

```

## RESULT 2

```

US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

```

```

Query Match      89.4%; Score 1460.5; DB 4; Length 312;
Best Local Similarity 90.1%; Pred. No. 5.1e-107;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

```

```

QY      1 MMTITPSFGAFLEIFNVKLLFAIPLVVFPYAAQAPMAEVOLVQSGGVERPGRSLRLS 60
Db      1 MMTITPSFGAFLEIFNVKLLFAIPLVVFPYAAQAPMAEVOLVQSGGVERPGRSLRLS 60
QY      61 CAASGTFDDYGSWROAPGKLEWVSGINMNGSGTGYADSVKGRVTTISRDAKNSLYL 120
Db      61 CAASGTFSSYGMWROAPGKLEWVAGIFDYGKKNYADSVKGRVTTISRDAKNSLYL 120

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```

QY      121 QNMSLRAEDTAVYYCA-----KIIAGAGRWYFDLMGKGTVTYVSSGGSGGGSGGSS 176
Db      121 QNMSLRAEDTAVYYCAKARDLLKVKGSSSGW-FDEWGRGTVTYVSSGGSGGGSGGSS 179
QY      177 ELTQDPVAVSVALCQTVRITCQGSLSRSYASWYQOKPGAPVLYTGKNNRPSGIDPRFS 236
Db      180 ELTQDPVAVSVALCQTVRITCQGSLSRSYASWYQOKPGAPVLYTGKNNRPSGIDPRFS 239
QY      237 GSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAE 296
Db      240 GSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAE 299
QY      297 QKLISEEDLINGAA 309
Db      300 QKLISEEDLINGAA 312

```

## RESULT 3

```

US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-11

```

```

Query Match      75.4%; Score 1231.5; DB 4; Length 310;
Best Local Similarity 78.0%; Pred. No. 4.4e-69;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

```

```

QY      1 MMTITPSFGAFLEIFNVKLLFAIPLVVFPYAAQAPMAEVOLVQSGGVERPGRSLRLS 60
Db      1 MMTITPSFGAFLEIFNVKLLFAIPLVVFPYAAQAPMAEVOLVQSGGVVQPGRSRLRLS 60
QY      61 CAASGTFDDYGSWROAPGKLEWVSGINMNGSGTGYADSVKGRVTTISRDAKNSLYL 120
Db      61 CAASGTFSSYGMWROAPGKLEWVAGIFDYGKKNYADSVKGRVTTISRDAKNSLYL 120
QY      121 QNMSLRAEDTAVYYCAKIIAGAGRWYFDLMGKGTVTYVSSGGSGGGSGGSSSELTQ 178
Db      121 QNMSLRAEDTAVYYCAR-----DRGYIMDYWGKGTITVTYVSSGGSGGGSGGSSQSVL 176

```



```

;
; NAME/KEY: DOMAIN
; LOCATION: (139)..(154)

```



---

Db 311 DSLSGWLFGGGTLTVL---RHNNHHH 334

RESULT 11

US-09-646-028-55

Sequence 55, Application US/09646028

Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Atya

TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 55

LENGTH: 339

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct.

US-09-646-028-55

Query Match

Best Local Similarity 49.7%; Score 811; DB 4; Length 339;

Best Local Similarity 61.0%; Pred. No. 4,1e-56;

Matches 163; Conservative 28; Mismatches 64; Indels 12; Gaps 5;

QY 33 AAOPAAAEVQVVGSGGVERPGGSLRLSCAASGFTTFDDYGMGSMVWRQAPKGLWVSGIMNW 92

Db 78 AQAAPKSLVEQLLESGLVQSGGSLRLSCVAGSLTFPSSAIIWVRQAPKGLWVSGISF 137

QY 93 NGSGCYAASVYGRVYISRDNAKNSLYLQMSLRADTVAYVYCAKILGAGRGVYFPLMKR 152

Db 138 SDDTYVADSVGRFSASDNSKNTVYLOMNLRPDVAVYFCAN--NOTGNECLDNWQ 195

QY 153 GTTVVSS-GGGSGGGSGGSGGS--SETLQDPVAVSALGQTVRITCOGDSLR--SY 205

Db 196 GTLVVSSKGGSGGSGGSGGSQSVLTQPPVSAPAGQRTVITSGGSSNIGAGVD 255

QY 206 ASWYQKPGQAPVLYLYGNRPSPGIPDRFSSSGSGNTASLTITGAQADEADYCNSSRD 265

Db 256 VMWYKFPETAKVLYISNNRPSGVPRFSGSGKSASLAITGLQLEDEGTYQCQND 315

QY 266 SSGNHVVRGGGTFKLTLYLGAHHHHH 292

Db 316 DSLSGWLFGGGTLTVL---RHNNHHH 339

RESULT 12

US-09-646-028-51

Sequence 51, Application US/09646028

Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Atya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 51

LENGTH: 348

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-51

Query Match

Best Local Similarity 49.3%; Score 805; DB 4; Length 348;

Best Local Similarity 61.9%; Pred. No. 1,3e-55;

Matches 161; Conservative 28; Mismatches 59; Indels 12; Gaps 5;

QY 40 EVQVVGSGGVERPGGSLRLSCAASGFTTFDDYGMGSMVWRQAPKGLWVSGIMNWGSTGY 99

Db 94 EVQLLESGLVQSGGSLRLSCVAGSLTFPSSAIIWVRQAPKGLWVSGISFSGDTVY 153

QY 100 ASVYGRVYISRDNAKNSLYLQMSLRADTVAYVYCAKILGAGRGVYFPLMKRTVYVS 159

Db 154 ADVYKRFASRDSKNTVYLOMNLRPDVAVYFCAN--NOTGNECLDNWQGTLYTVS 211

QY 160 S-GGGSGGGSGGSGGS--SETLQDPVAVSALGQTVRITCOGDSLR--SYASWYQK 212

Db 212 SRGGSGGGSGGSGGSQSVLTQPPVSAPAGQRTVITSGGSSNIGAGVDVWYQKF 271

QY 213 PGQAPVLYLYGNRPSPGIPDRFSSSGSGNTASLTITGAQADEADYCNSSRDSSGNHY 272

Db 272 PETAPKVLVYISNNRPSGVPRFSGSGKSASLAITGLQLEDEGTYQCQNDDSLGL 331

QY 273 FGGGTLTVLGAHHHHH 292

Db 332 FGGGTLTVL---RHNNHHH 348

RESULT 13

US-08-564-164A-2

Sequence 2, Application US/08564164A

Patent No. 6159947

GENERAL INFORMATION:

APPLICANT: Schweighofer, Fabien

APPLICANT: Tocque, Bruno

TITLE OF INVENTION: Intracellular Binding Proteins and Use

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

CITY: Collegetville

STATE: PA

COUNTRY: USA

ZIP: 19426-0107

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/564,164A

FILING DATE: 28-DEC-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00714

FILING DATE: 15-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93/07241

FILING DATE: 16-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Savitzky, Martin F.

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: ST93030-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)454-3816

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 284 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-564-164A-2

Query Match	49.2%;	Score 804;	DB 3;	Length 284;
Best Local Similarity	-59.8%;	Pred. NO. 1.2e-55;		
Matches 165;	Conservative 32;	Mismatches 65;	Indels 14;	Gaps 5;

Qy	33	AAOPAAAEVOLI	VOSGGGVYRRP	CGSGSRLTSCA	SGFFEDQYSW	ROAPRGKLE	VSGIN	92		
Db	21	AAOPAAAOVK	LDOOSGGGLV	PRSRSLKSC	VYSGFFSYG	INMIRQTP	RGKLEVA	ISS 80		
Qy	93	NGSGTGVADSV	KGRVITISRD	NKNSLYLQ	MNSLRAED	TAUYVCA	KILGAGRW	FYDLGK 152		
Db	81	GSSLYLAEV	TVAGRGFTIS	RDNAKNLYLQ	MTSLREDE	TAALYCA	RHNETHG	TD -FFDYWGQ 139		
Qy	153	GTVTVYSSG	GGSGGGSGGGSS	-ELRQDP-	AVSVALG	QIVVTRITCG	DSLSRYS	AWAYMQ 210		
Db	140	GTVTVYSSG	GGSGGGSGGGSDV	ELTQSPHS	LSASLGE	IVSYTECL	ASBGS	INYLAWQ 199		
Qy	211	QKPGAPV	LVLYGKNNR	PSGIPDR	FTSGSSSG	NTASLT	TGQAQADE	ADYYCNSR	DSGHN 270	
Db	200	QKPGKPOL	LIIYASSL	DDGVPS	RFRSGSGS	GTQPSL	KISMQ	PDDEG	YVYVCOQA	YKVPSS- 258
Qy	271	VVFGG	GTGLVGA	AAHHNNH	NGAEO	KLEISEED	LN 306			
Db	259	-TFGA	STKLEIKR	-----	-AAEO	KLEISEED	LN 284			

## RESULT 14

```

US-08-918-148-75
Sequence 75, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camella
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918.148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
LENGTH: 245
TYPE: PRY
ORGANISM: artificial
US-08-918-148-75

```

Query Match	48.1%;	Score 785.5;	DB 4;	Length 245;
Best Local Similarity	64.0%;	Pred. No. 2.8e-54;		
Matches 160;	Conservative 29;	Mismatches 54;	Indels 7;	Gaps 4;

QY	38	MAEVLVYSGGGGVERPGSLRLSCAASFFEDDYGMSVROAPGKGLGEMVSGIMNGGST	97
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	1	MAEVLVYSGGGGLVYPGSLRLSCAASFFTSDDYMSVIRAPGKGLGEMVSYISSSSTI	60
QY	98	GYADSVKGRVITISRDNAKNSLYLQNMSLRADDTAVYYCAKILGAGRGMYEDPLMGKITYT	157
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	61	YYADSVKGRFTISRDNSKNTLYLQNMSLRADDTAVYYCARMSGDA--FDIMQGIMVT	117
QY	158	VSSGGGGSGGGGGGGSS-ELTQDPA-VSVALQYVRLITQGSLSLYASMYQAKPGQ	215
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	118	VSSGGGGSGGGGGGGGGDLYWTFQSPSLTSLSVGDRAIITCRASEGITVHMLAWQAKPGK	177
		: : : : :     : : : : :     : : : : :     : : : : :	
QY	216	APLVLYYCKNNPPSGIPDRFSGSSSGNASTLTITGAQAEADVDYICRSDRSGNHVYFG	275
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	178	APRLIYTKASLSAAGAPSRPFSSGSGADFTLTISLQDPDPATYYC--QQYSNPLPLTFGG	235
QY	276	GTRKLYLGAA	285
		: : : : :	
Db	236	GTRLEVKRAA	245

RESULT 15  
US-08-918-148-76

```

? Sequence 76, Application US/08918148A
? Patent No. 6342320
? GENERAL INFORMATION:
? APPLICANT: Adams, Camella
? APPLICANT: W.
? APPLICANT: Carter, Paul J.
? APPLICANT: Fendly, Brian M.
? APPLICANT: Gurney, Austin L.
? TITLE OF INVENTION: Against Antibodi
? FILE REFERENCE: P0979
? CURRENT APPLICATION NUMBER: US/08/791
? CURRENT FILING DATE: 1997-08-25
? NUMBER OF SEQ ID NOS: 79
? SEQ ID NO 76
? LENGTH: 245
? TYPE: PRN
? ORGANISM: artificial
? US-08-918-148-76

```

Query Match	48.0%	Score 783.5	DB 4	Length 245
Best Local Similarity	63.3%	Pred. No. 4.1e-54		
Matches 159	Conservative 30	Mismatches 53	Indels 9	Gaps 5

QY	38	MAEVOIYOSGGGVEPBGSLRLSCAASFTFEDYCMWROAPGKGLEWVGGINNGSGST	97
Db	1	MAEVOIYOSGGGVQPGGSLSLSCASVSGTTLRTYGMHWROAPGKGLEWVAGISPEGRBE	60
QY	98	GYADSVKGRVITSRDANKSLYLONLSLRAEDTAVYYCAKILLAGRWY-FDLMGKTTV	156
Db	61	YYADSVKRFRTISRNSKNTLYLQNSLRAEDTAVYYCAR---DRSGTGMVWVGRTHY	116
QY	157	TVSSGGGSGGGSGSGGSS-ELTPDDPA-VSVALGOTPRITCGGSLRSYVASYWYOORKG	214
Db	117	TVSSGGGSGGGSGGGSGGSSDIQMTSPSTLSISIDRYTITCRASEGIIHMLAWYOORKG	176
QY	215	QAPVLYIYGNKRRPESGIPDRFSGSSSGNTASLTITGAQAEDEADYVCNSRDSGNNHYVG	274
Db	177	KAPKLLIYKASSLSAGAPRSFGSGSGTDFTLTISLPDPDFATYYC-QQYSNPPLFTG	234
QY	275	GGTCLTYVGAA 285	
Db	235	GKTLEILRAA 245	

Search completed: September 22, 2003, 15:16:00  
Job time : 19.2546 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 : Search time 51.7766 Seconds  
(without alignments)  
947.272 Million cell updates/sec

Title: US-10-052-798-9

Perfect score: 1633  
Sequence: 1 MTMTTSPGAFLEIFNVKK.....HHGCAEOKISEEDLNGAA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_19Jun03:\*

1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
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13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
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19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
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21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1633	100.0	309	20	AAW83322
2	1633	100.0	309	23	ABBO9603
3	1633	100.0	309	24	ABG74384
4	1460.5	89.4	312	20	AAW83323
5	1460.5	89.4	312	23	ABBO9604
6	1460.5	89.4	312	24	ABG74385
7	1279.5	78.4	277	23	ABG92019
8	1279.5	78.4	277	23	ABG78328
9	1275.5	78.1	277	23	ABG91841

10	1275.5	78.1	277	23	ABG78150	Human Fv molecule
11	1231.5	75.4	310	20	AAW83324	Single chain Apo-2
12	1231.5	75.4	310	23	ABBO9605	Amino acid sequenc
13	1231.5	75.4	310	24	ABG74386	Single chain antib
14	1223	74.9	266	23	ABG92020	Human antibody fra
15	1194.5	73.1	239	23	ABP46027	Human Blys binding
16	1189.5	72.8	239	23	ABP44926	Human Blys binding
17	1178.5	72.2	239	23	ABP46004	Human Blys binding
18	1178	72.1	246	23	ABG92026	Antibody protein #
19	1178	72.1	246	23	ABG78329	Human Fv molecule
20	1177	72.1	260	23	ABG92023	Antibody protein #
21	1171	71.7	256	23	ABG92025	Antibody biotag #1
22	1171	71.7	256	23	ABG78334	Human Fv molecule
23	1166.5	71.4	263	23	ABG92024	Antibody protein #
24	1155	70.7	282	23	AAE02185	PAM1 single chain
25	1139	69.7	240	23	ABP46002	Human Blys binding
26	1138	69.7	252	23	ABP45405	Human Blys binding
27	1133	69.4	238	21	AAI95198	Human Blys binding
28	1129	69.1	290	24	ABP55318	Anti-platelet gIyc
29	1122.5	68.7	239	23	ABP46012	Human Blys binding
30	1122	68.7	296	23	ABG60637	Immunoglobulin rel
31	1119	68.5	248	23	ABP45312	Human Blys binding
32	1118.5	68.5	291	23	AAE29202	Single chain antib
33	1116.5	68.4	239	23	ABP46011	Human Blys binding
34	1116.5	68.4	291	23	ABG60632	Immunoglobulin rel
35	1116	68.3	248	23	ABP44905	Human Blys binding
36	1116	68.3	248	23	ABP44909	Human Blys binding
37	1113.5	68.2	239	23	ABP46007	Human Blys binding
38	1113.5	68.2	249	23	ABP45324	Human Blys binding
39	1112	68.1	248	23	ABP44824	Human Blys binding
40	1112	68.1	248	23	ABP44903	Human Blys binding
41	1111.5	68.1	241	23	ABP45900	Human Blys binding
42	1109.5	67.9	243	23	ABP46045	Human Blys binding
43	1109.5	67.9	249	23	ABP44952	Human Blys binding
44	1109.5	67.9	251	23	ABP45729	Human Blys binding
45	1108.5	67.9	239	23	ABP46024	Human Blys binding

#### ALIGNMENTS

Result ID	Score	Query Match	Length	DB ID	Description
RESULT 1					
AAW83322					
AAW83322					standard; Protein; 309 AA.
AAW83322					
AAW83322					
16-MAR-1999					(first entry)
Single chain Apo-2 antibody 16E2.					
Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;					
tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;					
TNF cytokine.					
Homo sapiens.					
WO9851793-A1.					
19-NOV-1998.					
14-MAY-1998;					98WO-US09704.
09-FEB-1998;					98US-0020746.
15-MAY-1997;					97US-0857216.
(GETH ) GENENTECH INC.					
Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;					
WPI; 1999-045228/04.					
N-PSDB; AAV72532.					

PT Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

CC The present invention describes human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification. The present  
 CC sequence represents a single chain Apo-2 antibody, designated 16E2.

SQ Sequence 309 AA;

Query Match 100.0%; Score 1633; DB 20; Length 309;

Best Local Similarity 100.0%; Pred. No. 7.9e-101;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTIPSGAFLEINVKKLLFAIPLVVPFYAAPAMAEVOLVOSGGVERPGSLRLS 60  
 DB 1 MTMTIPSGAFLEINVKKLLFAIPLVVPFYAAPAMAEVOLVOSGGVERPGSLRLS 60  
 QY 61 CAASGTFDDYGSWVRQAPGKGLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120  
 DB 61 CAASGTFDDYGSWVRQAPGKGLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120  
 QY 121 QMNSLRADDTAVYYCAKILGAGRGWYFDLMGKTTYTVSSGGGSGGGSGSSSELTQ 180  
 DB 121 QMNSLRADDTAVYYCAKILGAGRGWYFDLMGKTTYTVSSGGGSGGGSGSSSELTQ 180  
 QY 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPVLYTGKNNRPSGIDPRFSGSSS 240  
 DB 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPVLYTGKNNRPSGIDPRFSGSSS 240  
 QY 241 GNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGSKTLVLGAANHHHHHGAADQKLI 300  
 DB 241 GNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGSKTLVLGAANHHHHHGAADQKLI 300  
 QY 301 SEEDLNGAA 309  
 DB 301 SEEDLNGAA 309  
 AC ABB09603;  
 AC ABB09603;  
 DT 29-MAY-2002 (first entry)  
 DE Amino acid sequence of single-chain Apo-2 antibody 16E2.  
 XX Human: Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
 XX caspase; apoptosis; cancer; antibody.  
 OS Bacteriophage.

XX US6342369-B1.  
 PN 29-JAN-2002.

XX 14-MAY-1998; 98US-0079029.

XX 15-MAY-1997; 97US-046615P.

XX 09-FEB-1998; 98US-074119P.

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ;

DR WPI: 2002-224941/28.

DR N-PDSB; ABL41733.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or  
 PT stimulating apoptosis in cancer cells, thus especially useful in the  
 PT treatment of cancer, or in enhancing immune-mediated cell death

XX Example 14; Fig 16; 68pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated  
 CC 16E2, which is isolated from a phage library. It is believed that  
 CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)  
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent  
 CC apoptosis and activating nuclear factor-kappa B. A soluble  
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2  
 CC antibodies may be used to activate or stimulate apoptosis in cancer  
 CC cells. They are therefore especially useful in the treatment of cancer,  
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to  
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in  
 CC affinity purification of Apo-2 from recombinant cell culture or natural  
 CC sources.

SQ Sequence 309 AA;

Query Match 100.0%; Score 1633; DB 23; Length 309;

Best Local Similarity 100.0%; Pred. No. 7.9e-101;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTIPSGAFLEINVKKLLFAIPLVVPFYAAPAMAEVOLVOSGGVERPGSLRLS 60  
 DB 1 MTMTIPSGAFLEINVKKLLFAIPLVVPFYAAPAMAEVOLVOSGGVERPGSLRLS 60  
 QY 61 CAASGTFDDYGSWVRQAPGKGLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120  
 DB 61 CAASGTFDDYGSWVRQAPGKGLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120  
 QY 121 QMNSLRADDTAVYYCAKILGAGRGWYFDLMGKTTYTVSSGGGSGGGSGSSSELTQ 180  
 DB 121 QMNSLRADDTAVYYCAKILGAGRGWYFDLMGKTTYTVSSGGGSGGGSGSSSELTQ 180  
 QY 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPVLYTGKNNRPSGIDPRFSGSSS 240  
 DB 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPVLYTGKNNRPSGIDPRFSGSSS 240  
 QY 241 GNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGSKTLVLGAANHHHHHGAADQKLI 300  
 DB 241 GNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGSKTLVLGAANHHHHHGAADQKLI 300  
 QY 301 SEEDLNGAA 309  
 DB 301 SEEDLNGAA 309  
 AC ABG74384;  
 AC ABG74384;  
 DT ABG74384 standard; Protein; 309 AA.  
 DE Human: Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
 XX caspase; apoptosis; cancer; antibody.  
 OS Bacteriophage.

DT 11-APR-2003 (first entry)  
XX Single chain antibody (scfv) fragment 16E2.  
XX  
XX Apo-2: tumour necrosis factor family; TNFR; gene therapy;  
KM apoptosis; tissue-specific typing; affinity purification;  
KM competitive-type receptor binding assay; mouse; 16E2.  
XX  
XX Mus sp.  
XX US2002150985-A1.  
XX  
XX 17-OCT-2002.  
XX  
XX 02-NOV-2001; 2001US-0052798.  
XX  
XX 15-MAY-1997; 97US-046615P.  
PR 09-FEB-1998; 98US-074119P.  
PR 14-MAY-1998; 98US-0079029.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX WPI; 2003-198287/19.  
DR N-PSDB; ABX16407.  
XX  
XX New Apo-2 polypeptides and polynucleotides, useful for inducing  
PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in  
PT quantitative diagnostic assays, or in generating antibodies against  
PT Apo-2 -  
XX  
XX Example 14; Fig 16; 64pp; English.  
XX  
XX The invention describes a novel isolated Apo-2 polypeptide. The Apo-2  
CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo  
CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control  
CC against samples containing unknown quantities of Apo-2, in generating  
CC antibodies, in affinity purification techniques, and in competitive-type  
CC receptor binding assays when labelled with, for instance, radioiodine,  
CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
CC diagnostic for tissue-specific typing. This is the amino acid sequence  
CC of the single chain antibody fragment (scfv) 16E2 used in the  
CC preparation of anti-apo-2 antibodies.  
XX  
XX Sequence 309 AA;  
SQ  
Query Match 100.0%; Score 1633; DB 24; Length 309;  
Best Local Similarity 100.0%; Pred. No. 7.9e-101;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPYAOPMAAEVOLVOSGGVPRPGSLRLS 60  
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPYAOPMAAEVOLVOSGGVPRPGSLRLS 60  
QY 61 CAASGFTFDDYGMNVQAPKGLKLEWVSGIMNMGSGTGYADSVKGRYTIISDNKNSLYL 120  
DB 61 CAASGFTFDDYGMNVQAPKGLKLEWVSGIMNMGSGTGYADSVKGRYTIISDNKNSLYL 120  
QY 121 QMNSLRADPTAVYICAKILGAGRWYFDLMGKGTTVVSSGGSGSGSGSSSELTQ 180  
DB 121 QMNSLRADPTAVYICAKILGAGRWYFDLMGKGTTVVSSGGSGSGSGSSSELTQ 180  
QY 181 DPAVSVALGOTVITCGDLSRSYYASWYQKPGOAPLVLYGKNNRPSGIPDRFSSSS 240  
DB 181 DPAVSVALGOTVITCGDLSRSYYASWYQKPGOAPLVLYGKNNRPSGIPDRFSSSS 240  
QY 241 GNTASLTITGAQAEDEADYVCNSRDSSGNHVFFGGGKTLTVLGAAGAHNNHNGAEOKLI 300  
DB 241 GNTASLTITGAQAEDEADYVCNSRDSSGNHVFFGGGKTLTVLGAAGAHNNHNGAEOKLI 300  
QY 301 SEEDLNGAA 309  
DB 301 SEEDLNGAA 309  
|||||||

DB 301 SEEDLNGAA 309  
RESULT 4  
ID AAW83323 standard; Protein: 312 AA.  
XX AAW83323;  
XX  
XX 16-MAR-1999 (first entry)  
XX  
XX Single chain Apo-2 antibody 20E6.  
DE  
XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
KM tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
KM TNF cytokine.  
XX  
XX Homo sapiens.  
XX  
XX WO9851793-A1.  
XX  
XX 19-NOV-1998.  
PD  
XX 14-MAY-1998; 98WO-US09704.  
PE  
XX 09-FEB-1998; 98US-0020746.  
PR 15-MAY-1997; 97US-0857216.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX WPI; 1999-045228/04.  
DR N-PSDB; AAV72533.  
XX  
XX Human Apo-2 polypeptide inducing apoptosis - useful to treat  
PT conditions linked with decreased apoptosis e.g. cancer, and produce  
PT antibodies to increase or decrease apoptosis  
XX  
XX Example 14; Fig 16; 134pp; English.  
XX  
XX The present invention describes human Apo-2. Apo-2 can be used  
CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
CC to treat conditions associated with decreased apoptosis e.g. cancer.  
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
CC can be used to identify agents activating Apo-2, useful to treat  
CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
CC therapeutically (e.g. those containing immunoglobulin sequences can be  
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
CC antibodies). It can be used to produce antibodies which can be combined  
CC with a (particularly pharmaceutically acceptable) carrier in compositions  
CC or used to produce dimeric molecules (especially homodimeric molecules  
CC comprising first and second Apo-2 antibodies). Agonistic (especially  
CC single-chain) antibodies can be administered to induce apoptosis in  
CC mammalian cancer cells, and antagonistic antibodies used to block  
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
CC antibodies may also be used diagnostically e.g. to detect Apo-2  
CC expression in cells/tissues and in Apo-2 purification. The present  
CC sequence represents a single chain Apo-2 antibody, designated 20E6.  
XX  
SQ Sequence 312 AA;  
Query Match 89.4%; Score 1460.5; DB 20; Length 312;  
Best Local Similarity 90.1%; Pred. No. 2.2e-89;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;  
QY 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPYAOPMAAEVOLVOSGGVPRPGSLRLS 60  
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPYAOPMAAEVOLVOSGGVPRPGSLRLS 60  
|||||||





CC antibodies, in affinity purification techniques, and in competitive-type  
CC receptor binding assays when labelled with, for instance, radiiodine,  
CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
CC diagnostic for tissue-specific typing. This is the amino acid sequence  
CC of the single chain antibody fragment (scFv) 20E6 used in the  
CC preparation of anti-apo-2 antibodies.

XX Sequence 312 AA;

Query Match 89.4%; Score 1460.5; DB 24; Length 312;  
Best Local Similarity 90.1%; Pred. No. 2.2e-89;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTSPFGAFLEIFNVKKLLFAIPLVPEYAAQPMAMAEVQLVQSGGVERPGSLRLS 60  
DB 1 MTMTSPFGAFLEIFNVKKLLFAIPLVPEYAAQPMAMAEVQLVQSGGVERPGSLRLS 60  
QY 61 CAAGGFTFDYGMWVQAPGKGLWVSGIMWNGSGTGYADSVKGRVTISDNKAKNSLYL 120  
DB 61 CAAGGFTFDYGMWVQAPGKGLWVSGIMWNGSGTGYADSVKGRVTISDNKAKNSLYL 120  
QY 121 QMNSLRADPAVYVYCA---KILGAGRGWYFDLWKGKTVTVSSGGSGSGSGSGSS 176  
DB 121 QMNSLRADPAVYVYCA---KILGAGRGWYFDLWKGKTVTVSSGGSGSGSGSGSS 176  
QY 121 QMNSLRADPAVYVYCA---KILGAGRGWYFDLWKGKTVTVSSGGSGSGSGSGSS 179  
DB 121 QMNSLRADPAVYVYCA---KILGAGRGWYFDLWKGKTVTVSSGGSGSGSGSGSS 179  
QY 177 ELTQDPAPVVALGQTVRITCGDSLRSYYSWYQKPGQAPVLYTYGKNNRPGSIPDRFS 236  
DB 177 ELTQDPAPVVALGQTVRITCGDSLRSYYSWYQKPGQAPVLYTYGKNNRPGSIPDRFS 236  
QY 180 ELTQDPAPVVALGQTVRITCGDSLRSYYSWYQKPGQAPVLYTYGKNNRPGSIPDRFS 239  
DB 180 ELTQDPAPVVALGQTVRITCGDSLRSYYSWYQKPGQAPVLYTYGKNNRPGSIPDRFS 239  
QY 237 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTKLVGAAAHNHHGAAE 296  
DB 237 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTKLVGAAAHNHHGAAE 296  
QY 240 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTKLVGAAAHNHHGAAE 299  
DB 240 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTKLVGAAAHNHHGAAE 299  
QY 297 OKLISEEDLNGAA 309  
DB 297 OKLISEEDLNGAA 312

RESULT 7  
ABG92019 ID ABG92019 standard; Protein: 277 AA.

XX ABG92019;  
XX 04-DEC-2002 (first entry)

DE Human antibody fragment #203.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
KW reticentosis; leukaemia; inflammatory disease; cardiovascular disease;  
KW myocardial infarction; retinopathic disease; abnormal platelet function;  
KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX MO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US49442.

XX 29-DEC-2000; 2000US-258948P.

XX 29-DEC-2000; 2000US-0751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
PI Szenthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer

PS Claim 23; Page 308-309; 310pp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, reticentosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,  
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
CC increasing mortality of tumour or leukaemia cells, for increasing the  
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
CC or anti-leukaemia agents, or for decreasing the number of tumour or  
CC leukaemia cells in a patient, or in the manufacture of a medicament for  
CC the above mentioned purposes. The epitopes are useful for diagnosing and  
CC treating diseases such as cancer, leukaemia, autoimmune diseases,  
CC inflammatory diseases, cardiovascular diseases such as myocardial  
CC infarction, retinopathic diseases and other diseases mediated by abnormal  
CC platelet function and diseases caused by sulphated tyrosine-dependent  
CC protein-protein interactions. This sequence represents a human antibody  
CC fragment of the invention.

SO Sequence 277 AA;

Query Match 78.4%; Score 1279.5; DB 23; Length 277;  
Best Local Similarity 90.6%; Pred. No. 2e-77;  
Matches 251; Conservative 4; Mismatches 7; Indels 15; Gaps 3;

QY 33 AADPAMAEVOLVQSGGVERPGSLRLSCAAGTFFPDYGMWVQAPGKLEWVSGINW 92  
DB 16 AADPAMAEVOLVQSGGVERPGSLRLSCAAGTFFPDYGMWVQAPGKLEWVSGINW 92  
QY 93 NGSGTGYADSVKGRVTISDNKAKNSLYLQMSLRAEDPAVYVYCAKILGAGWYFDLWKG 152  
DB 76 NGSGTGYADSVKGRVTISDNKAKNSLYLQMSLRAEDPAVYVYCAKILGAGWYFDLWKG 152  
QY 153 GTTVTVSSGGSGSGSGSGSELTPDPAVVALGQTVRITCGDSLRSYYSWYQK 212  
DB 130 GTTVTVSSGGSGSGSGSGSELTPDPAVVALGQTVRITCGDSLRSYYSWYQK 212  
QY 213 PGQAPVLYTYGKNNRPGSIPDRFSGSSGNTASLTITTAQAEDEADYYCNSRDSGNNHV 272  
DB 190 PGQAPVLYTYGKNNRPGSIPDRFSGSSGNTASLTITTAQAEDEADYYCNSRDSGNNHV 249  
QY 273 FGGGKTLTVGAAAHNHHGAAEOKLISEEDLNGAA 309  
DB 250 FGGGKTLTVGAAAHNHHGAAEOKLISEEDLNGAA 277

RESULT 8  
ABG78328 ID ABG78328 standard; Protein: 277 AA.

XX ABG78328;

XX 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #203.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
KW disulfide Fv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

XX MO200259264-A2.

XX Novel isolated epitope present on cancer cells and important in

PD 01-AUG-2002.  
XX  
XX 31-DEC-2001; 2001WO-US49440.  
PF  
XX 29-DEC-2000; 2000US-0751181.  
XX  
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.  
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;  
PI Plaksin D, Peretz T;  
XX  
XX WPI: 2002-619166/66.  
DR N-PSDB; ABS63384.  
XX  
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favour of other  
PT cells -  
XX  
XX Claim 141; Fig 14; 232pp; English.  
XX  
XX The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the Leukaemia cell is an  
CC acute myeloid Leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention.  
XX  
SQ Sequence 277 AA:  
  
Query Match 78.4%; Score 1279.5; DB 23; Length 277;  
Best Local Similarity 90.6%; Pred. No. 2e-77;  
Matches 251; Conservative 4; Mismatches 7; Indels 15; Gaps 3;  
  
QY 33 AAQPMAMAEVOLVOSGGGVRRPGSLRLSCAASGFTFDDYGMGSMVROAPKGLGEMWSGIMW 92  
DB 16 AAQPMAMAEVOLVOSGGGVRRPGSLRLSCAASGFTFDDYGMGSMVROAPKGLGEMWSGIMW 75  
QY 93 NGSGTGYADSVKGRVYISRDNAKNSLYLQMSLRAEDTAVVYCAKILGAGRGWYFDLWGK 152  
DB 76 NGSGTGYADSVKGRVYISRDNAKNSLYLQMSLRAEDTAVVYCAKILGAGRGWYFDLWGK 129  
QY 153 GTTVTVSSGGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQOK 212  
DB 130 GTLVTVSSRGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQOK 189  
QY 213 PGQAPVLYLYGKNNRPSGIPDRFSSSSGNTASLTITGAQADEADYYCNSRSDSSGNHYV 272  
DB 190 PGQAPVLYLYGKNNRPSGIPDRFSSSSGNTASLTITGAQADEADYYCNSRSDSSGNHYV 249  
QY 273 FCGGTRKLTLYGAAGAAHHHHHGAEOKLISEEDLNGAA 309  
DB 250 FCGGTRKLTLYGA-----AABOKLISEEDLNGAA 277

XX Human: antibody; epitope; cancer; tumour; cell rolling; inflammation;  
KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
KW myocardial infarction; retinopathic disease; abnormal platelet function;  
KW sulphated tyrosine-dependent protein-protein interaction.  
XX  
XX Homo sapiens.  
XX  
XX WO200253700-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 31-DEC-2001; 2001WO-US49442.  
XX  
XX 29-DEC-2000; 2000US-258948P.  
PR 29-DEC-2000; 2000US-0751181.  
XX  
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.  
XX  
XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
PI Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
XX  
XX WPI: 2002-674776/72.  
XX  
XX Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer -  
XX  
PS Claim 23; Page 233-234; 310pp; English.  
XX  
XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,  
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
CC increasing mortality of tumour or leukaemia cells, for increasing the  
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
CC or anti-leukaemia agents, or for decreasing the number of tumour or  
CC leukaemia cells in a patient, or in the manufacture of a medicament for  
CC the above mentioned purposes. The epitopes are useful for diagnosing and  
CC treating diseases such as cancer, leukaemia, autoimmune diseases,  
CC inflammatory diseases, cardiovascular diseases such as myocardial  
CC infarction, retinopathic diseases and other diseases mediated by abnormal  
CC platelet function and diseases caused by sulphated tyrosine-dependent  
CC protein-protein interactions. This sequence represents a human antibody  
CC fragment of the invention.  
XX  
SQ Sequence 277 AA:  
  
Query Match 78.1%; Score 1275.5; DB 23; Length 277;  
Best Local Similarity 89.9%; Pred. No. 3.7e-77;  
Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;  
  
QY 33 AAQPMAMAEVOLVOSGGGVRRPGSLRLSCAASGFTFDDYGMGSMVROAPKGLGEMWSGIMW 92  
DB 16 AAQPMAMAEVOLVOSGGGVRRPGSLRLSCAASGFTFDDYGMGSMVROAPKGLGEMWSGIMW 75  
QY 93 NGSGTGYADSVKGRVYISRDNAKNSLYLQMSLRAEDTAVVYCAKILGAGRGWYFDLWGK 152  
DB 76 NGSGTGYADSVKGRVYISRDNAKNSLYLQMSLRAEDTAVVYCAKILGAGRGWYFDLWGK 129  
QY 153 GTTVTVSSGGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQOK 212  
DB 130 GTLVTVSSRGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQOK 189  
QY 213 PGQAPVLYLYGKNNRPSGIPDRFSSSSGNTASLTITGAQADEADYYCNSRSDSSGNHYV 272

Db 190 PGQAPVLYIGKNNRPSGIPDRFSSSSGNTASLITITGAQAEADYICNSRDSSGNHV 249  
 Qy 273 FGGGTKLTVLGAHHHHHGAAROKLISEEDLNGAA 309  
 Db 250 FGGGKLTVLGA-----AAEQKLISEEDLNGAA 277

RESULT 10  
 ABG78150  
 ID ABG78150 standard; Protein: 277 AA.  
 AC ABG78150;  
 DT 15-NOV-2002 (first entry)  
 XX Human Fv molecule hypervariable region related peptide #25.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 OS Homo sapiens.  
 PN WO200259264-A2.  
 XX 01-AUG-2002.  
 PD 31-DEC-2001; 2001WO-US49440.  
 XX 29-DEC-2000; 2000US-0751181.  
 PR (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plakstin D, Peretz T;  
 XX WPI: 2002-619166/66.  
 DR WPI: 2002-619166/66.  
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favour of other  
 PT cells -  
 PS Claim 4; Page 155-156; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention.

XX Sequence 277 AA:  
 SO  
 Query Match 78.1%; Score 1275.5; DB 23; Length 277;  
 Best Local Similarity 89.9%; Pred. No. 3.7e-77;  
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

Qy 33 AAGPAAAEVLYVGGGVERGSLRSCASGTFPDYGSWVRQARGLKLEWVSGINW 92  
 Db 16 AAGPAAAEVLYVGGGVERGSLRSCASGTFPDYGSWVRQARGLKLEWVSGINW 75  
 Qy 93 NGSGTYADSVKGVHTTISRDNKNSLYLQNNSLRAEDTAVYCAKILGAGRGWFDLMGK 152

Db 76 NGSGTYADSVKGVHTTISRDNKNSLYLQNNSLRAEDTAVYCAKILGAGRGWFDLMGK 129  
 Qy 153 GTTYVSSGGGGGGGGGGSSSLTDDPAVSVALGQVTRTCGDSLRYSYASWYQOK 212  
 Db 130 GTLYVSSRGGGGGGGGGGSSSLTDDPAVSVALGQVTRTCGDSLRYSYASWYQOK 189  
 Qy 213 PGQAPVLYIGKNNRPSGIPDRFSSSSGNTASLITITGAQAEADYICNSRDSSGNHV 272  
 Db 190 PGQAPVLYIGKNNRPSGIPDRFSSSSGNTASLITITGAQAEADYICNSRDSSGNHV 249

Qy 273 FGGGTKLTVLGAHHHHHGAAROKLISEEDLNGAA 309  
 Db 250 FGGGKLTVLGA-----AAEQKLISEEDLNGAA 277

RESULT 11  
 AAW83324  
 ID AAW83324 standard; Protein: 310 AA.  
 AC AAW83324;  
 DT 16-MAR-1999 (first entry)  
 XX Single chain Apo-2 antibody 24C4.  
 DE Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
 KW TNF cytokine.  
 OS Homo sapiens.  
 PN WO9851793-A1.  
 XX 19-NOV-1998.  
 PD 14-MAY-1998; 98WO-US09704.  
 XX 09-FEB-1998; 98US-0020746.  
 PR 15-MAY-1997; 97US-0857216.  
 XX (GETH ) GENENTECH INC.  
 PA Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
 PI WPI: 1999-045228/04.  
 DR N-PSDB; AAV72534.  
 XX Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis  
 PS Example 14; Fig 16; 134pp; English.

XX The present invention describes human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2

expression in cells/tissues and in Apo-2 purification. The present sequence represents a single chain Apo-2 antibody, designated 24C4.

SQ Sequence 310 AA;

Query Match 75.4%; Score 1231.5; DB 20; Length 310;

Best Local Similarity 78.0%; Pred. No. 3.5e-74; Mismatches 40; Indels 9; Gaps 4;

Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

```

OY 1 MTMTSPGAFPLEIFNNKLLFAIPLVVFFYAAPAPAMEVOLVDSGGGVERRPGSLRLS 60
DB 1 MTMTSPGAFPLEIFNNKLLFAIPLVVFFYAAPAPAMEVOLVDSGGGVERRPGSLRLS 60
OY 61 CAASGTFDDYGMASVWRQAPRGKGLVWVGGINNNGSGTGADSVKGRVTSRDNANKSLYL 120
DB 61 CAASGTFESSYGMHWRQAPRGKGLVWVAGIFYDGKNKYADSVKGRFTISRDNANKSLYL 120
OY 121 QNNSLRAEPTAVYACAKILGAGRWYF-DLMGKGTTVVYSSGGSGSGSGSGGS-SEL 178
DB 121 QNNSLRAEPTAVYACAR---DRGYTMDVWGKGTTVVYSSGGSGSGSGSGGSQSVL 176
OY 179 TDDPAVSVALGQTVRTTCGDSLR--SYASMYOQKPGQAPVLVYIGKNRPSGIPDRF 235
DB 177 TQPPVSAGAPGQRTVISTGRSSNIGAGHDVHMVQQLPETAARKLLIDDSNRPSPVDRF 236
OY 236 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFEGGTRKLVLAGAANHHNHGAA 295
DB 237 SGRSGTASLSLTITGAQAEDEADYYCQSYDSSLRSGSVFGGTRKLVLAGAANHHNHGAA 296
OY 296 EOKLISEEDLNGAA 309
DB 297 EOKLISEEDLNGAA 310

```

#### RESULT 12

ABR09605 ID ABR09605 standard; Protein; 310 AA.

XX ABR09605;

DT 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 24C4.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;

OS Bacteriophage.

PN US6342369-B1.

PD 29-JAN-2002.

PF 14-MAY-1998; 98US-0079029.

PR 15-MAY-1997; 97US-046615P.

PR 09-FEB-1998; 98US-074119P.

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ;

DR WPI; 2002-224941/28.

DR N-PSDB; ABL41735.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or

PT stimulating apoptosis in cancer cells; thus especially useful in the

PT treatment of cancer, or in enhancing immune-mediated cell death

XX Example 14; Fig 16; 68pp; English.

XX The present sequence represents a single-chain Apo-2 antibody, designated

CC 24C4, which is isolated from a phage library. It is believed that

CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)

CC family. Apo-2 polypeptide is capable of triggering caspase-dependent

CC apoptosis and activating nuclear factor-kappa B. A soluble

CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2

CC antibodies may be used to activate or stimulate apoptosis in cancer

CC cells. They are therefore especially useful in the treatment of cancer,

CC to enhance immune-mediated cell death in cells expressing Apo-2, to

CC detect expression of Apo-2 in specific cells, tissues or serum, and in

CC affinity purification of Apo-2 from recombinant cell culture or natural

CC sources.

SQ Sequence 310 AA;

Query Match 75.4%; Score 1231.5; DB 23; Length 310;

Best Local Similarity 78.0%; Pred. No. 3.5e-74;

Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

```

OY 1 MTMTSPGAFPLEIFNNKLLFAIPLVVFFYAAPAPAMEVOLVDSGGGVERRPGSLRLS 60
DB 1 MTMTSPGAFPLEIFNNKLLFAIPLVVFFYAAPAPAMEVOLVDSGGGVERRPGSLRLS 60
OY 61 CAASGTFDDYGMASVWRQAPRGKGLVWVGGINNNGSGTGADSVKGRVTSRDNANKSLYL 120
DB 61 CAASGTFESSYGMHWRQAPRGKGLVWVAGIFYDGKNKYADSVKGRFTISRDNANKSLYL 120
OY 121 QNNSLRAEPTAVYACAKILGAGRWYF-DLMGKGTTVVYSSGGSGSGSGSGGS-SEL 178
DB 121 QNNSLRAEPTAVYACAR---DRGYTMDVWGKGTTVVYSSGGSGSGSGSGGSQSVL 176
OY 179 TDDPAVSVALGQTVRTTCGDSLR--SYASMYOQKPGQAPVLVYIGKNRPSGIPDRF 235
DB 177 TQPPVSAGAPGQRTVISTGRSSNIGAGHDVHMVQQLPETAARKLLIDDSNRPSPVDRF 236
OY 236 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFEGGTRKLVLAGAANHHNHGAA 295
DB 237 SGRSGTASLSLTITGAQAEDEADYYCQSYDSSLRSGSVFGGTRKLVLAGAANHHNHGAA 296
OY 296 EOKLISEEDLNGAA 309
DB 297 EOKLISEEDLNGAA 310

```

#### RESULT 13

ABG74386 ID ABG74386 standard; Protein; 310 AA.

XX ABG74386;

DT 11-APR-2003 (first entry)

XX Single chain antibody (scFv) fragment 24C4.

XX Apo-2; tumour necrosis factor family; TNFR; gene therapy;

XX apoptosis; tissue-specific typing; affinity purification;

XX competitive-type receptor binding assay; mouse; 24C4.

OS Mus sp.

PN US2002150985-A1.

PD 17-OCT-2002.

PF 02-NOV-2001; 2001US-0052798.

PR 15-MAY-1997; 97US-046615P.

PR 09-FEB-1998; 98US-074119P.

PR 14-MAY-1998; 98US-0079029.

PA (GETH ) GENENTECH INC.

PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;

DR WPI; 2003-198287/19.

DR	N-PSDB:ABX16409.
XX	
PT	New Apo-2 polypeptides and polynucleotides, useful for inducing
PT	apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
PT	quantitative diagnostic assays, or in generating antibodies against
PT	Apo-2
XX	
PS	Example 14; Fig 16; 64pp; English.
XX	
CC	The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
CC	polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
CC	or ex vivo gene therapy, in quantitative diagnostic assays, as a control
CC	against samples containing unknown quantities of Apo-2, in generating
CC	antibodies, in affinity purification techniques, and in competitive-type
CC	receptor binding assays when labelled with, for instance, radiolodine,
CC	enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
CC	diagnostic for tissue-specific typing. This is the amino acid sequence
CC	of the single chain antibody fragment (scFv) 24C4 used in the
CC	preparation of anti-apo-2 antibodies.
XX	
SQ	Sequence 310 AA;
	Query Match 75.4%; Score 1231.5; DB 24; Length 310;
	Best Local Similarity 78.0%; Pred. No.3.5e-74;
	Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4
OY	1 MTMTPSGAFLLEFNFKLLFAFLPLVVPFYFAADPAMAENVLOVSGGVERPGSLRLS 60
DB	1 MTMTTPSGAFLLEFNFKLLFAFLPLVVPFYFAADPAMAENVLOVSGGCVDPGSLRLS 60
OY	61 CAASGTFDDYGMVMWRQAPGKGLBWSGIMNNGSGTGADSVKGRVTISRMANSLYL 120
DB	61 CAASGFISVSGMHWVRQAPGKGLBWSVAGIFYDGNKYUADSVKGRFTISRDNKNTLYL 120
OY	121 QMNSLRADTAVYVYAKILGAGRGYF-DLMCKGTITYVSSGGSGSGSGSGS-SEL 178
DB	121 QMNSLRADTAVYVYAKILGAGRGYF-DRGYYMDVWCKGTITYVSSGGSGSGSGSGSQSYL 176
OY	179 TDPPAVSALACTVATTCOGDSLRL---SYLASWYQOKPQAQVULIYGNKNRPSGIPDRF 235
DB	177 TOPPSVSAAPQORVITISCTGRSNIGAGHDVIMYQDLRGTARKLLIYDSSNRPSCVPRDF 236
OY	236 SGSSSGNTASLTITGAQADEADYUCNSRDSGSHNVFEGGATKLYLGAADNNHNGAA 295
DB	237 SGSRGTSASLALITGLQADEADYUCQSYDSSLRSQVSGGKTVYLGAADNNHNGAA 296
OY	296 EOKLISEEDLNGAA 309
DB	297 EOKLISEEDLNGAA 310
	RESULT 14
ID	ABG92020 standard; Protein; 266 AA.
AC	ABG92020;
XX	
DT	04-DEC-2002 (first entry)
XX	
DE	Human antibody fragment #204.
XX	
KM	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM	metastasis; hypervariable region; autoimmune disease; thrombosis;
KM	restenosis; leukemia; inflammatory disease; cardiovascular disease;
KM	myocardial infarction; retinopathic disease; abnormal platelet function;
XX	sulphated tyrosine-dependent protein-protein interaction.
OS	Homo sapiens.
XX	
PN	WO200253700-A2.
XX	
PD	11-JUL-2002.
XX	

```

PF 31-DEC-2001; 2001MO-US49442.
XX
XX 29-DEC-2000; 2000US-258948P.
PR 29-DEC-2000; 2000US-0751181.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
PA
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nlmod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI: 2002-674776/72.
DR
XX Novel isolated epitope present on cancer cells and important in
XX PT physiological phenomena such as cell rolling, metastasis and
XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX PT diseases, and cancer
XX
XX Disclosure: Page 309-310; 310pp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
XX CC important in physiological phenomena such as cell rolling, metastasis and
XX CC inflammation, where the epitope is capable of being bound by an antibody,
XX CC its antigen-binding fragment or its complex comprising at least one
XX CC antibody or its binding fragment having a first hypervariable region. The
XX CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
XX CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
XX CC tumour or leukaemia cells, increase in number of tumour or leukaemia
XX CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
XX CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
XX CC increasing mortality of tumour or leukaemia cells, for increasing the
XX CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
XX CC or anti-leukaemia agents, or for decreasing the number of tumour or
XX CC leukaemia cells in a patient, or in the manufacture of a medicament for
XX CC the above mentioned purposes. The epitopes are useful for diagnosing and
XX CC treating diseases such as cancer, leukaemia, autoimmune diseases,
XX CC inflammatory diseases, cardiovascular diseases such as myocardial
XX CC infarction, retinopathic diseases and other diseases mediated by abnormal
XX CC platelet function and diseases caused by sulphated tyrosine-dependent
XX CC protein-protein interactions. This sequence represents a human antibody
XX CC fragment of the invention.
XX
XX Sequence 266 AA:
SQ
XX
XX Query Match 74.9%; Score 1223; DB 23; Length 266;
XX Best Local Similarity 92.5%; Pred. No. 1,1e-73;
XX Matches 235; Conservative 5; Mismatches 8; Indels 6; Gaps 1
XX
XX 33 AAQPAAAEVOLVQSGGGERPGSLRLSCAASGFTPDYGMGMVRAQAPGKLEWYSGINW 92
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 16 AAQPAAAEVOLVESGGVVRPGSLRLSCAASGFTPDYGMGMVRAQAPGKLEWYSGINW 75
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 93 NGSGTGYADSVKGRYTISRDNAAKNSLYLQMSLRADETRAVYCAKILGAGRWYTDLMCK 152
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 76 NGSGTGYADSVKGRFTISRDNAAKNSLYLQMSLRADETRAVYCAKMRAP-----VIMQ 129
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 153 GTTVVSSGGGSGGSGGSSSELTODPAVSAVALGOTVRITTCGDSLRSYYASMYQOK 212
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 130 GTLVTVSSNGGGSGGSGGSSSELTODPAVSAVALGOTVRITTCGDSLRSYYASMYQOK 189
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 213 PGQAEVLVIYGNKNNPSCGIPDFSGSSSGNTASLITTGQAQADEADYVYCNRSDDSGNHVY 272
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX DB 190 PGQAEVLVIYGNKNNPSCGIPDFSGSSSGNTASLITTGQAQADEADYVYCNRSDDSGNHVY 249
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX QY 273 FGGGTKLTIVLGAA 286
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX DB 250 FGGGTKLTIVLGAA 263
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX
XX RESULT 15
XX ABP46027
XX ID ABP46027 standard; Protein: 239 AA.
XX
XX ABP46027:

```

XX 19-AUG-2002 (first entry)  
XX  
XX Human Blys binding scFv SEQ ID 2038.  
DE  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
PN  
XX  
XX 10-JAN-2002.  
PD  
XX  
XX 15-JUN-2001; 2001WO-US19110.  
PF  
XX  
XX 16-JUN-2000; 2000US-212210P.  
PR  
XX 17-OCT-2000; 2000US-240816P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 21-MAR-2001; 2001US-277379P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI  
XX  
XX WPI; 2002-114799/15.  
DR  
XX  
XX  
XX Antibodies against B lymphocyte stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
PT  
XX  
XX  
XX Claim 1: Page 2830-2831; 3148pp: English.  
PS  
XX  
XX  
XX

CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
XX  
SQ Sequence 239 AA;

Query Match 73.1%; Score 1194.5; DB 23; Length 239;  
Best Local Similarity 93.4%; Pred. No. 7.6e-72;  
Matches 228; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 40 EVOLVQSGGGERPGSGSLRLSCAASGFTPEDDYGMSSWVRQAPGKLEWYSGINMGSGSTGY 99  
DB 1 EYQLVESGGGVYRPGSGSLRLSCAASGFTPEDDYGMSSWVRQAPGKLEWYSGINMGSGSTGY 60  
QY 100 ADSVAGRTYISRDNAKNSLYLQMSLRADDTAVYYCAKTLGAGRGWYEDLMGKGTTVYS 159  
DB 61 ADSVAGRTYISRDNAKNSLYLQMSLRADDTAVYYCAR-----RRYALDYMGQGLTVYS 115  
QY 160 SGGGSGGGGGSSGSSSELTQDPAVSVALGQTVRITCGDSLSRYASWYQKPGQAPVL 219  
DB 116 SGGGSGGGGGSSGSSSELTQDPAVSVALGQTVRITCGDSLSRYASWYQKPGQAPVL 175

QY 220 VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGGTRL 279  
DB 176 VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGGTRL 235  
QY 280 TVLG 283  
DB 236 TVLG 239

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Job time : 52.7766 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:16:07 : Search time 34.1858 Seconds  
(without alignments)  
1345.823 Million cell updates/sec

Title: US-10-052-798-9

Perfect score: 1633  
Sequence: 1 MTMTPTSFCAFFLEIFNVKK.....HHHCAPQKLTSEEDLNGAA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1633	100.0	309	12	US-10-288-917-9
2	1633	100.0	309	14	US-10-052-798-9
3	1460.5	89.4	312	12	US-10-288-917-10
4	1460.5	89.4	312	14	US-10-052-798-10
5	1231.5	75.4	310	12	US-10-288-917-11
6	1231.5	75.4	310	14	US-10-052-798-11
7	1194.5	73.1	239	11	US-09-880-748-2038
8	1189.5	72.8	239	11	US-09-880-748-937
9	1178.5	69.7	239	11	US-09-880-748-2015
10	1139	69.7	240	11	US-09-880-748-2013
11	1138	69.7	252	11	US-09-880-748-1416
12	1129	69.1	290	12	US-09-969-748C-2
13	1129	69.1	290	12	US-09-949-039-2
14	1122.5	68.7	239	11	US-09-880-748-2023
15	1122	68.7	296	12	US-09-969-748C-12

16	1122	68.7	296	12	US-09-949-039-75
17	1119	68.5	248	11	US-09-880-748-1323
18	1116.5	68.4	239	11	US-09-880-748-2022
19	1116	68.3	248	11	US-09-880-748-916
20	1116	68.3	248	11	US-09-880-748-920
21	1113.5	68.2	239	11	US-09-880-748-2018
22	1113.5	68.2	249	11	US-09-880-748-1335
23	1112	68.1	248	11	US-09-880-748-835
24	1112	68.1	248	11	US-09-880-748-911
25	1111.5	67.9	243	11	US-09-880-748-2036
26	1109.5	67.9	249	11	US-09-880-748-963
27	1109.5	67.9	251	11	US-09-880-748-1740
28	1109.5	67.9	239	11	US-09-880-748-2035
29	1108.5	67.9	251	11	US-09-880-748-952
30	1108.5	67.9	243	11	US-09-880-748-1929
31	1105.5	67.7	243	11	US-09-880-748-996
32	1102.5	67.5	249	11	US-09-880-748-1109
33	1102.5	67.5	245	11	US-09-880-748-1826
34	1101.5	67.5	247	11	US-09-880-748-1764
35	1101.5	67.5	251	11	US-09-880-748-908
36	1101.5	67.5	251	11	US-09-880-748-982
37	1101.5	67.5	246	11	US-09-880-748-1975
38	1101	67.4	247	11	US-09-880-748-1703
39	1099.5	67.3	243	11	US-09-880-748-1942
40	1098.5	67.3	247	11	US-09-880-748-924
41	1098.5	67.3	248	11	US-09-880-748-913
42	1098	67.2	237	11	US-09-880-748-2039
43	1097.5	67.2	237	11	US-09-880-748-2112
44	1097.5	67.2	237	11	US-09-880-748-2112
45	1096.5	67.1	243	11	US-09-880-748-1940

## ALIGNMENTS

RESULT 1  
US-10-288-917-9  
: Sequence 9, Application US/10288917  
: Publication No. US20030148455A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/288,917  
FILING DATE: 06-NOV. US20030148455A1-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/052798  
FILING DATE: 02-NOV-2001  
APPLICATION NUMBER: 09/079029  
FILING DATE: 14-MAY-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-FEB-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.

Sequence 75, Appl	1
Sequence 1323, Ap	2
Sequence 2022, Ap	3
Sequence 916, App	4
Sequence 920, App	5
Sequence 2018, Ap	6
Sequence 1335, Ap	7
Sequence 835, App	8
Sequence 914, App	9
Sequence 1911, Ap	10
Sequence 2056, Ap	11
Sequence 963, App	12
Sequence 1740, Ap	13
Sequence 2035, Ap	14
Sequence 922, App	15
Sequence 1929, Ap	16
Sequence 982, App	17
Sequence 1975, Ap	18
Sequence 1703, Ap	19
Sequence 1826, Ap	20
Sequence 1764, Ap	21
Sequence 908, App	22
Sequence 924, App	23
Sequence 913, App	24
Sequence 2039, Ap	25
Sequence 2112, Ap	26
Sequence 1940, Ap	27

```

1      REGISTRATION NUMBER: 35,600
2      REFERENCE/DOCKET NUMBER: P1101R2D1C1
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: 650/225-5416
5      TELEFAX: 650/952-9881
6      INFORMATION FOR SEQ ID NO: 9:
7      SEQUENCE CHARACTERISTICS:
8      LENGTH: 309 amino acids
9      TYPE: Amino Acid
10     TOPOLOGY: Linear
11     US-10-288-917-9
12     SEQUENCE DESCRIPTION: SEQ ID NO: 9:
13
14     Query Match      100.0%; Score 1633; DB 12; Length 309;
15     Best Local Similarity 100.0%; Pred. No. 8.5e-108;
16     Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0
17
18     QY      1 MTMTTPSGAFLELEFNKKLLFAIPLVVPFYAAQAPAAAEVOLVSGGSGVERPGGSLRLS 60
19     DB      1 MTMTTPSGAFLELEFNKKLLFAIPLVVPFYAAQAPAAAEVOLVSGGSGVERPGGSLRLS 60
20     QY      61 CAASGFTTDDYGMKSVROAPGKGLIEWSGIMNNGSGTGYADSVKGRVTISRDNANKSLYL 120
21     DB      61 CAASGFTTDDYGMKSVROAPGKGLIEWSGIMNNGSGTGYADSVKGRVTISRDNANKSLYL 120
22     QY      121 QMNSLRADTAVYYCAKILGAGRGVFPDMCKGTIVTVSSGGSGSGGSGGSSSELTQ 180
23     DB      121 QMNSLRADTAVYYCAKILGAGRGVFPDMCKGTIVTVSSGGSGSGGSGGSSSELTQ 180
24     QY      181 DPAAVSVALGQTVRTICQGDLSRSYASYAQKPGQAPLVITYGKNNRPSGIPDRFGSSS 240
25     DB      181 DPAAVSVALGQTVRTICQGDLSRSYASYAQKPGQAPLVITYGKNNRPSGIPDRFGSSS 240
26     QY      241 GNTASLTITGAQAEDEADYCNRSRDSGNHYVFGGKTLVYLGAAAHNHHHGAEOKLI 300
27     DB      241 GNTASLTITGAQAEDEADYCNRSRDSGNHYVFGGKTLVYLGAAAHNHHHGAEOKLI 300
28     QY      301 SEEDLNGAA 309
29     DB      301 SEEDLNGAA 309
30
31     RESULT 2
32     US-10-052-798-9
33     Sequence 9, Application US/10052798
34     Publication No. US20020150985A1
35     GENERAL INFORMATION:
36     APPLICANT: Adams, Camilia W.
37     Ashkenazi, Avi J.
38     Chuntharapai, Anan
39     Kim, Kyung J.
40     TITLE OF INVENTION: Apo-2 Receptor
41     NUMBER OF SEQUENCES: 14
42     CORRESPONDENCE ADDRESS:
43     ADDRESSEE: Genentech, Inc.
44     STREET: 1 DNA Way
45     CITY: South San Francisco
46     STATE: California
47     COUNTRY: USA
48     ZIP: 94080
49     COMPUTER READABLE FORM:
50     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
51     COMPUTER: IBM PC compatible
52     OPERATING SYSTEM: PC-DOS/MS-DOS
53     SOFTWARE: Winpatin (Genentech)
54     CURRENT APPLICATION DATA:
55     APPLICATION NUMBER: US/10/052,798
56     FILING DATE: 02-NO. US20020150985A1-2001
57     CLASSIFICATION: <Unknown>
58     PRIOR APPLICATION DATA:
59     APPLICATION NUMBER: US/09/079,029
60     FILING DATE: <Unknown>
61     ATTORNEY/AGENT INFORMATION:

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1      NAME: Marschang, Diane L.
2      REGISTRATION NUMBER: 35,600
3      REFERENCE/DOCKET NUMBER: P1101R2
4      TELECOMMUNICATION INFORMATION:
5          TELEPHONE: 650/225-5416
6          TELEFAX: 650/952-9881
7      INFORMATION FOR SEQ ID NO: 9:
8          SEQUENCE CHARACTERISTICS:
9              LENGTH: 309 amino acids
10             TYPE: Amino Acid
11             TOPOLOGY: Linear
12      US-10-052-798-9
13      SEQUENCE DESCRIPTION: SEQ ID NO: 9:
14
15      Query Match          100.0%; Score 1633; DB 14; Length 309;
16      Best Local Similarity 100.0%; Pred. NO. 8.5e-108;
17      Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0
18
19      Oy      1  MMTITTSFGAFLEIINVKKLLFAIPLVVPYFAAOPAMAEEVOLVOSGGVYRPGSGSLRLS 60
20      Db      1  MTMTTTSFGAFLEIINVKKLLFAIPLVVPYFAAOPAMAEEVOLVOSGGVYRPGSGSLRLS 60
21
22      Oy      61  CAASGFTFPDYGSMWVROAPGKGLBWSGIMNNGSGTGADSVKGRYTIISDNKNSLYL 120
23      Db      61  CAASGFTFPDYGSMWVROAPGKGLBWSGIMNNGSGTGADSVKGRYTIISDNKNSLYL 120
24
25      Oy      121  QMNSLRAEDTAYIYCAKILGAGRGVFPDLMKGGTIVYSSGGGSGGGSGGSSSLTQ 180
26      Db      121  QMNSLRAEDTAYIYCAKILGAGRGVFPDLMKGGTIVYSSGGGSGGGSGGSSSLTQ 180
27
28      Oy      181  DPAVSVALGOTYRITCGDSLRSXYAASWYQKPGQAPVLVYUGKNNRPSCGIPDRFSGSSS 240
29      Db      181  DPAVSVALGOTYRITCGDSLRSXYAASWYQKPGQAPVLVYUGKNNRPSCGIPDRFSGSSS 240
30
31      Oy      241  GINASTLITIGAQAEDADADYYCNSRDSGNNHVFGGGTGLTVLGAADNNHHNGAAEQKLI 300
32      Db      241  GINASTLITIGAQAEDADADYYCNSRDSGNNHVFGGGTGLTVLGAADNNHHNGAAEQKLI 300
33
34      Oy      301  SEEDLNGAA 309
35      Db      301  SEEDLNGAA 309
36
37      RESULT 3
38      US-10-288-917-10
39      ; Sequence 10, Application US/10288917
40      ; Publication No. US20030148455A1
41      GENERAL INFORMATION:
42      APPLICANT: Adams, Camilla W.
43          Ashkenazi, Avi J.
44          Chuntharapai, Anan
45          Kim, Kyung J.
46      TITLE OF INVENTION: Apo-2 Receptor
47      NUMBER OF SEQUENCES: 14
48      CORRESPONDENCE ADDRESS:
49          ADDRESSEE: Genentech, Inc.
50          STREET: 1 DNA Way
51          CITY: South San Francisco
52          STATE: California
53          COUNTRY: USA
54          ZIP: 94080
55      COMPUTER READABLE FORM:
56      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
57      COMPUTER: IBM PC compatible
58      OPERATING SYSTEM: PC-DOS/MS-DOS
59      SOFTWARE: Winpatin (Genentech)
60      CURRENT APPLICATION DATA:
61      APPLICATION NUMBER: US/10/288,917
62      FILING DATE: 06-NO. US20030148455A1-2002
63      CLASSIFICATION: <Unknown>
64      PRIOR APPLICATION DATA:
65      APPLICATION NUMBER: 10/052798
66      FILING DATE: 02-NOV-2001

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APPLICATION NUMBER: 09/079029  
FILING DATE: 14-MAY-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-FEB-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-288-917-10

Query Match 89.4%; Score 1460.5; DB 12; Length 312;  
Best Local Similarity 90.1%; Pred. No. 1.2e-95;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;  
QY 1 MTMTSPGAFLEIFNVKLLFAIPLVVPFYAOPAMAEVOLVOSGGVERPGSLRLS 60  
DB 1 MTMTSPGAFLEIFNVKLLFAIPLVVPFYAOPAMAGVOLVBSGGGLVPGGSLRLS 60  
QY 61 CAASGTFDDYGMWVROAPGKGLWVSGINNNGSTGYADSVKGRVTTISRDNAKSLYL 120  
DB 61 CAASGTFESSYMWVROAPGKGLWVANI KODGSEKYYVDSVKGRFTISRDNAKSLYL 120  
QY 121 QNNSLRAPEDTAVYYCA---KILGAGRGVFDLMKGTIVTVSSGGSGSGSGSGSS 176  
DB 121 QNNSLRAPEDTAVYYCARDLLKVGSSSGW-FDPWGRGTVTVSSGGSGSGSGSGSS 179  
QY 177 ELTOPAVVALGQVTRITCOGDSLRSYASWYQKPGQAPLVITGKNNRPSGIPDRS 236  
DB 180 ELTOPAVVALGQVTRITCOGDSLRSYASWYQKPGQAPLVITGKNNRPSGIPDRS 239  
QY 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTVLGAANHHNHGAAE 296  
DB 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTVLGAANHHNHGAAE 299  
QY 297 OKLISEEDLNGAA 309  
DB 300 OKLISEEDLNGAA 312

## RESULT 4

US-10-052-798-10  
Sequence 10, Application US/10052798  
Publication No. US20020150985A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/052, 798  
FILING DATE: 02-NO. US20020150985A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/079, 029  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-052-798-10

Query Match 89.4%; Score 1460.5; DB 14; Length 312;  
Best Local Similarity 90.1%; Pred. No. 1.2e-95;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;  
QY 1 MTMTSPGAFLEIFNVKLLFAIPLVVPFYAOPAMAEVOLVOSGGVERPGSLRLS 60  
DB 1 MTMTSPGAFLEIFNVKLLFAIPLVVPFYAOPAMAGVOLVBSGGGLVPGGSLRLS 60  
QY 61 CAASGTFDDYGMWVROAPGKGLWVSGINNNGSTGYADSVKGRVTTISRDNAKSLYL 120  
DB 61 CAASGTFESSYMWVROAPGKGLWVANI KODGSEKYYVDSVKGRFTISRDNAKSLYL 120  
QY 121 QNNSLRAPEDTAVYYCA---KILGAGRGVFDLMKGTIVTVSSGGSGSGSGSGSS 176  
DB 121 QNNSLRAPEDTAVYYCARDLLKVGSSSGW-FDPWGRGTVTVSSGGSGSGSGSGSS 179  
QY 177 ELTOPAVVALGQVTRITCOGDSLRSYASWYQKPGQAPLVITGKNNRPSGIPDRS 236  
DB 180 ELTOPAVVALGQVTRITCOGDSLRSYASWYQKPGQAPLVITGKNNRPSGIPDRS 239  
QY 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTVLGAANHHNHGAAE 296  
DB 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTVLGAANHHNHGAAE 299  
QY 297 OKLISEEDLNGAA 309  
DB 300 OKLISEEDLNGAA 312

## RESULT 5

US-10-288-917-11  
Sequence 11, Application US/10288917  
Publication No. US20030148455A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/288.917  
FILING DATE: 06-Nov-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 10/052798  
FILING DATE: 02-Nov-2001  
APPLICATION NUMBER: 09/079029  
FILING DATE: 14-May-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-Feb-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-288-917-11

Query Match 75.4%; Score 1231.5; DB 12; Length 310;  
Best Local Similarity 78.0%; Pred. No. 1.7e-79;  
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;  
QY 1 MMTITPFGAFLEINNVKLLFAIPLVVPEYAAOPAMAEVOLVOSGGVERGSLRLS 60  
DB 1 MMTITPFGAFLEINNVKLLFAIPLVVPEYAAOPAMAEVOLVOSGGVERGSLRLS 60  
QY 61 CAASGFTFDYGSWVROAPKGLKLEWVSGINMGSGTGYADSVKGRVTTISRDNAKNSLYL 120  
DB 61 CAASGFTFSSYGHMWRQAPKGLKLEWVAGIFDYGKMYADSVKGRFTISRDNKNTLYL 120  
QY 121 QMNSLAEDTAVYYCAKILGAGRWTF-DLMGKGTIVTVSSGGGSGGGSGGGG-SEL 178  
DB 121 QMNSLAEDTAVYYCAR---DRGYIYMDVMGKGTIVTVSSGGGSGGGSGGGGSOVL 176  
QY 179 TOPPAVALGQVTRITCGDSLRL---SYASWYQKPGQAPVLYTVGKNNRPSGIPDRF 235  
DB 179 TOPPAVALGQVTRITCGSSNIGAGHDVHWYQDLPGRAPKLLIYDSSNRPSGVPRF 236  
QY 236 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGKTLVYLGAAAHNNHNGAA 295  
DB 237 SGSRSGTSASLTITGAQAEDEADYCYQSYDSSLRGSVFGGKTVTVLGAAAHNNHNGAA 296  
QY 296 EOKLISEEDLNGAA 309  
DB 297 EOKLISEEDLNGAA 310

RESULT 6  
US-10-052-798-11  
Sequence 11, Application US/10052798  
Publication No. US20020150985A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/052.798  
FILING DATE: 02-Nov-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/079.029  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-052-798-11

Query Match 75.4%; Score 1231.5; DB 14; Length 310;  
Best Local Similarity 78.0%; Pred. No. 1.7e-79;  
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;  
QY 1 MMTITPFGAFLEINNVKLLFAIPLVVPEYAAOPAMAEVOLVOSGGVERGSLRLS 60  
DB 1 MMTITPFGAFLEINNVKLLFAIPLVVPEYAAOPAMAEVOLVOSGGVERGSLRLS 60  
QY 61 CAASGFTFDYGSWVROAPKGLKLEWVSGINMGSGTGYADSVKGRVTTISRDNAKNSLYL 120  
DB 61 CAASGFTFSSYGHMWRQAPKGLKLEWVAGIFDYGKMYADSVKGRFTISRDNKNTLYL 120  
QY 121 QMNSLAEDTAVYYCAKILGAGRWTF-DLMGKGTIVTVSSGGGSGGGSGGGG-SEL 178  
DB 121 QMNSLAEDTAVYYCAR---DRGYIYMDVMGKGTIVTVSSGGGSGGGSGGGGSOVL 176  
QY 179 TOPPAVALGQVTRITCGDSLRL---SYASWYQKPGQAPVLYTVGKNNRPSGIPDRF 235  
DB 179 TOPPAVALGQVTRITCGSSNIGAGHDVHWYQDLPGRAPKLLIYDSSNRPSGVPRF 236  
QY 236 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGKTLVYLGAAAHNNHNGAA 295  
DB 237 SGSRSGTSASLTITGAQAEDEADYCYQSYDSSLRGSVFGGKTVTVLGAAAHNNHNGAA 296  
QY 296 EOKLISEEDLNGAA 309  
DB 297 EOKLISEEDLNGAA 310

RESULT 7  
US-09-880-748-2038  
Sequence 2038, Application US/09880748  
Publication No. US2003005937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880.748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212.210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240.816  
PRIOR FILING DATE: 2000-10-17

;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO: 2038  
;; LENGTH: 239  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-2038

Query Match 73.1%; Score 1194.5; DB 11; Length 239;  
Best Local Similarity 93.4%; Pred. No. 5.4e-77;  
Matches 228; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 99  
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Db 1 EVOLVESGGGVVRPGGSLRLSCAASGFTDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 60  
QY 100 ADSVKGRTISRDNAKNSLYLQMNSLRADDTAVYCAKILGARGVYFDLMKGTITYVS 159  
|||||  
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRADDTAVYCAR-----RRALDYWGQGLTYVS 115  
QY 160 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYYASWYQKPGQAPVL 219  
|||||  
Db 116 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYYASWYQKPGQAPVL 175  
QY 220 VIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVFGGGRTL 279  
|||||  
Db 176 VIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVFGGGRTL 235  
QY 280 TVLG 283  
|||||  
Db 236 TVLG 239

RESULT 8  
US-09-880-748-937  
;; Sequence 937, Application US/09880748  
;; Publication No. US20030059937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; CURRENT FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO: 937  
;; LENGTH: 239  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-937

Query Match 72.8%; Score 1189.5; DB 11; Length 239;  
Best Local Similarity 93.0%; Pred. No. 1.2e-76;  
Matches 227; Conservative 4; Mismatches 8; Indels 5; Gaps 1;  
QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 99  
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Db 1 EVOLVESGGGVVRPGGSLRLSCAASGFTDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 60  
QY 100 ADSVKGRTISRDNAKNSLYLQMNSLRADDTAVYCAKILGARGVYFDLMKGTITYVS 159  
|||||  
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRADDTAVYCAR-----RRALDYWGQGLTYVS 115  
QY 160 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYYASWYQKPGQAPVL 219  
|||||  
Db 116 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYYASWYQKPGQAPVL 175  
QY 220 VIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVFGGGRTL 279  
|||||  
Db 176 VIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVFGGGRTL 235  
QY 280 TVLG 283  
|||||  
Db 236 TVLG 239

RESULT 9  
US-09-880-748-2015  
;; Sequence 2015, Application US/09880748  
;; Publication No. US20030059937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; CURRENT FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO: 2015  
;; LENGTH: 239  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-2015

Query Match 72.2%; Score 1178.5; DB 11; Length 239;  
Best Local Similarity 91.8%; Pred. No. 7.3e-76;  
Matches 224; Conservative 7; Mismatches 8; Indels 5; Gaps 1;

QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 99  
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Db 1 EVOLVESGGGVVRPGGSLRLSCAASGFTDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 60  
QY 100 ADSVKGRTISRDNAKNSLYLQMNSLRADDTAVYCAKILGARGVYFDLMKGTITYVS 159  
|||||  
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRADDTAVYCAR-----RRALDYWGQGLTYVS 115  
QY 160 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYYASWYQKPGQAPVL 219  
|||||  
Db 116 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYYASWYQKPGQAPVL 175  
QY 220 VIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVFGGGRTL 279  
|||||  
Db 176 VIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVFGGGRTL 235  
QY 280 TVLG 283  
|||||  
Db 236 TVLG 239

RESULT 10

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US-09-880-748-2013
; Sequence 2013, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2013

Query Match          69.7%; Score 1139; DB 11; Length 240;
Best Local Similarity 89.3%; Pred. No. 4,5e-73;
Matches 218; Conservative 10; Mismatches 12; Indels 4; Gaps 1;

QY 40 EVOLVSGGGERPGSLRLSCAASGFTPDYGMHWRAQPGKLEWVSGINNGSGTGY 99
   :|||||: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSYINSGSTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 100 ADVKGRFTISRANKSLYLQNNSLRAEDTAVYYCAKILGARGWTFDLMGKTYTVS 159
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVKGRFTISRANKSLYLQNNSLRAEDTAVYYCAK---KRYFDWGRGTWTVS 116
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QY 160 SGGGSGGGSGGGSSSELTQDPAVSYALGQTVRITCGDSLRSYASWYQKPGQAPVL 219
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 SGGGSGGGSGGGSSSELTQDPAVSYALGQTVRITCGDSLRSYASWYQKPGQAPVL 176
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VYIKNNRPSGIDPRFSGSSSGNTASITTTGAQAEDEADYYCNSRSSGHHVFGGKTKL 279
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 VYIKNNRPSGIDPRFSGSSSGNTASITTTGAQAEDEADYYCNSRSSGHHVFGGKTKL 236
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QY 280 TVLG 283
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Db 237 TVLG 240
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RESULT 11
US-09-880-748-1416
; Sequence 1416, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
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SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1416
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1416

Query Match          69.7%; Score 1138; DB 11; Length 252;
Best Local Similarity 86.9%; Pred. No. 5,5e-73;
Matches 219; Conservative 11; Mismatches 14; Indels 8; Gaps 2;

QY 40 EVOLVSGGGERPGSLRLSCAASGFTPDYGMHWRAQPGKLEWVSGINNGSGTGY 99
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Db 1 EVOLVSGGGLVQPGSLRLSCAASGFTDEYAMHWRAQPGKLEWVSGISWNSGLAY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 100 ADVKGRFTISRANKSLYLQNNSLRAEDTAVYYCAKILG-----AGRWTF--DLWG 151
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Db 61 ADVKGRFTISRANKSLYLQNNSLRAEDTAVYYCAKDRGVGVDLTGRTYYGADVWG 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 152 KFTTVYSSGGSGGGSGGSELTPDPVAVSALGQTVRITCGDSLRSYASWYQ 211
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 QRTWTVYSSGGSGGGSGGSELTPDPVAVSALGQTVRITCGDSLRSYASWYQ 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 212 KPGQAPVLYLYGKNNRPSGIDPRFSGSSSGNTASITTTGAQAEDEADYYCNSDSSGNNY 271
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KPGQAPVLYLYGKNNRPSGIDPRFSGSSSGNTASITTTGAQAEDEADYYCNSDSSGNNY 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 272 VFGGKTKLYLG 283
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Db 241 VFGGKTKLYLG 252
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RESULT 12
US-09-969-748C-2
; Sequence 2, Application US/09969748C
; Publication No. US20030161809A1
; GENERAL INFORMATION:
; APPLICANT: ARIZKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; APPLICANT: BASU, Anatesh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACT
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969,748C
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-748C-2

Query Match          69.1%; Score 1129; DB 12; Length 290;
Best Local Similarity 80.1%; Pred. No. 2,8e-72;
Matches 226; Conservative 18; Mismatches 20; Indels 18; Gaps 4;

QY 33 AAQPAMA-----EVOLVSGGGERPGSLRLSCAASGFTPDYGMHWRAQPGKLEWV 87
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Db 16 AAQPAMADYKAKOVOLVSGGGLVQPGSLRLSCAASGFTFSYAMHWRAQPGKLEWV 75
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 88 SGIMNGSGTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVVYCAKILGAGRGWYF 147  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 76 SAISGSGSTYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVVYCAR---DTRG-YF 131  
QY 148 DLAKGTTVYVSSGGGSGGGGSSSELTODPAVSVALGQTVRITCQDSLRSYYAS 207  
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Db 132 DLMRGTLTVVSSGGGSGGGGSSSELTODPAVSVALGQTVRITCQDSLRSKYHAS 191  
QY 208 WYQKPGCAPLVYVYGNKNRPSGIPDRFSSSGSNTASLTITGAQAEDEADYVYCNRSRDS 267  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 192 WYQKPGCAPLVYVYGNKNRPSGIPDRFSSSGTSGDTASLTITGAQAEDEADYVYCHSRDSN 251  
QY 268 GNHYVFGGKTLVYLGAAAHNHNHGAEAQKLISEEDLNGAA 309  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 252 ADLVVFGGKTVYVLGA-----AAEQKLISEEDLNGAA 284

RESULT 13  
US-09-949-039-2  
; Sequence 2, Application US/09949039  
; Publication No. US20030166160A1  
; GENERAL INFORMATION:  
; APPLICANT: HAWLEY, STEPHEN B.  
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE  
; BINDING OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS  
; FILE REFERENCE: 057220/1301  
; CURRENT APPLICATION NUMBER: US/09/949, 039  
; CURRENT FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 290  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: psyn5AF amino  
; OTHER INFORMATION: acid sequence  
US-09-949-039-2

Query Match 69.1%; Score 1129; DB 12; Length 290;  
Best Local Similarity 80.1%; Pred. No. 2.8e-72;  
Matches 226; Conservative 18; Mismatches 20; Indels 18; Gaps 4;  
QY 33 AAOPAMA-----EVLVQSGGVERPGSLRLSCAASGFTFDDYGMWVROAPGKLEWY 87  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 16 AAGPAMADYKAKQVLQVQSGGVVQPGSLRLSCAASGFTTSSYAMHWVROAPGKLEWY 75  
QY 88 SGIMNGSGTGYADSVKGRVTISRDNKNSLYLQMNSLRAEDTAVVYCAKILGAGRGWYF 147  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 76 SAISGSGSTYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVVYCAR---DTRG-YF 131  
QY 148 DLAKGTTVYVSSGGGSGGGGSSSELTODPAVSVALGQTVRITCQDSLRSYYAS 207  
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Db 132 DLMRGTLTVVSSGGGSGGGGSSSELTODPAVSVALGQTVRITCQDSLRSKYHAS 191  
QY 208 WYQKPGCAPLVYVYGNKNRPSGIPDRFSSSGSNTASLTITGAQAEDEADYVYCNRSRDS 267  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 192 WYQKPGCAPLVYVYGNKNRPSGIPDRFSSSGTSGDTASLTITGAQAEDEADYVYCHSRDSN 251  
QY 268 GNHYVFGGKTLVYLGAAAHNHNHGAEAQKLISEEDLNGAA 309  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 252 ADLVVFGGKTVYVLGA-----AAEQKLISEEDLNGAA 284

RESULT 14  
US-09-880-748-2023  
; Sequence 2023, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruden et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: P5523  
; CURRENT APPLICATION NUMBER: US/09/880, 748

; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2023  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2023

Query Match 68.7%; Score 1122.5; DB 11; Length 239;  
Best Local Similarity 89.0%; Pred. No. 6.5e-72;  
Matches 218; Conservative 8; Mismatches 12; Indels 7; Gaps 2;  
QY 40 EVOLVQSGGVERPGSLRLSCAASGFTFDDYGMWVROAPGKLEWVSGIMNGSGTGY 99  
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Db 1 QVQLQESGGGVVQPGGSLRLSCAASGFTFSYGHWVROAPGKLEWVSALISGSGSTYY 60  
QY 100 ADSVKGRVTISRDNKNSLYLQMNSLRAEDTAVVYCAKILGAGRG-WTFDLAKGTTVTV 158  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVVYCA-----RDADAFEDWGGGTWTV 114  
QY 159 SSGGGSGGGSGGGGSSSELTODPAVSVALGQTVRITCQDSLRSYYASWYQKPGCAPV 218  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 115 SSGGGSGGGSGGGGSSSELTODPAVSVALGQTVRITCQDSLRSYYASWYQKPGCAPV 174  
QY 219 LVYIGKNRPSGIPDRFSSSGSNTASLTITGAQAEDEADYVYCNRSRDSGNHYVFGGKTK 278  
| : : ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
Db 175 LVYIGKNRPSGIPDRFSSSGSNTASLTITGAQAEDEADYVYCHSRDSNGNHYVFGGKTK 234  
QY 279 LTVVG 283  
| : : |||||  
Db 235 LTVLG 239

RESULT 15  
US-09-969-748C-12  
; Sequence 12, Application US/09969748C  
; Publication No. US20030161809A1  
; GENERAL INFORMATION:  
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou, L.  
; APPLICANT: SHERIDAN, Phillip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven  
; APPLICANT: BASU, Amareesh  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE  
; FILE REFERENCE: 057220-0303  
; CURRENT APPLICATION NUMBER: US/09/969, 748C  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 296



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 20.9098 Seconds  
(without alignments)  
1421.159 Million cell updates/sec

Title: US-10-052-798-9  
Perfect score: 1633  
Sequence: 1 MTMTPTSGAFLEIFNVKK.....HHGAPQKLISEEDLNGAA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	44.1	268	2	A56446
2	571.5	35.0	249	2	S41374
3	568	34.8	109	2	S19663
4	562	34.4	108	2	S47184
5	551.5	33.8	110	2	S36272
6	546	33.4	121	2	S31104
7	546	33.4	127	2	S70444
8	541	33.1	108	2	S38498
9	539	33.0	109	2	S38496
10	531.5	32.5	233	2	JC5322
11	530	32.3	233	1	S25748
12	527	32.3	108	1	L3HUSH
13	518.5	31.8	110	2	S19672
14	517.5	31.7	146	2	S02083
15	509	31.2	123	2	S30532
16	503.5	30.8	128	2	S31595
17	503	30.8	96	2	S36060
18	503	30.8	115	2	S13726
19	503	30.8	120	2	S36273
20	503	30.8	121	2	S31118
21	502	30.7	138	2	S31666
22	502	30.7	233	2	S25741
23	498.5	30.5	120	2	S44111
24	498	30.5	119	2	S31107
25	494	30.3	98	2	S26928
26	492	30.1	119	2	C36005
27	491.5	30.1	128	2	S26790
28	491	30.1	160	2	S05271
29	489.5	30.0	112	2	PH1654

30	488.5	29.9	145	2	S11239	Ig heavy chain V r
31	485	29.7	140	2	S31686	Ig heavy chain V r
32	482.5	29.5	120	2	S48798	Ig heavy chain V r
33	482	29.5	123	2	S31114	Ig heavy chain - h
34	481	29.5	119	2	D36005	Ig heavy chain V r
35	480.5	29.4	140	2	S70442	Ig heavy chain pre
36	480	29.4	140	2	S19666	Ig heavy chain V r
37	480	29.4	140	2	S31588	Ig heavy chain V r
38	479.5	29.4	147	2	S17780	Ig variable region
39	476	29.1	119	2	S31108	Ig heavy chain - h
40	473	29.0	127	2	S38489	Ig heavy chain - h
41	470.5	28.8	141	2	S31105	Ig heavy chain (su
42	470.5	28.8	118	2	S31669	Ig heavy chain V r
43	469.5	28.8	120	2	E49590	Ig heavy chain V r
44	469	28.7	120	2	S36278	Ig heavy chain V r
45	468	28.7	121	2	I55673	Ig heavy chain - h

ALIGNMENTS

RESULT 1  
A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide  
A:Reference number: A56446; MUID:95229583; PMID:7713873  
A:Accession: A56446  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match 44.1%; Score 720; DB 2; Length 268;  
Best Local Similarity 53.6%; Pred. No. 5.3e-41;  
Matches 147; Conservative 38; Mismatches 81; Indels 8; Gaps 5;

QY	38	MAEVLVDSGGGVEPRGSLRLSCAASGFTPDYGMVWROAPGKLEWVGMINNGST	97
DB	1	MAQVKLOESGAELVPRGASVKLTCTTSGFNKIDTYMHVKKQRPDGLMIGHRIAPANGIT	60
QY	98	GYADSVKGRVITISRDNAKNSLYLQNNSLRADDAVYCAKILGAGRGVYFDLMGKGTVT	157
DB	61	KYDPKFGKATIAADTSSNTAVYLQLSLTSEDTAVYCYASYLTR--YENVWGQTTVT	117
QY	158	VSSGGGSGGGSGGGSGSS-ELTODPAY-SVALGQTVRITQGDLSRSTYASWVOQRQO	215
DB	118	VSSGGGSGGGSGGSDSGGSDIELTOSPALMSASLGRKVMSCRRASSSV-FLYVQQRKSDA	176
QY	216	APLVITYKNNRPSSGIPRFGSSSGNTASLTITGAEDADYVACNSRDNGNHNVPVG	275
DB	177	SPKLWVYTTSHLPREVPRPFRSGSGGNGSYSLTISMEEDADATYYCOQFTSS--PFTGGS	234
QY	276	GTKLITVLGAHAHHHHHNGAEOKLISEEDLNGAA	309
DB	235	GTKLEIKRSAHHHHHNGAEOKLISEEDLNGAA	268

RESULT 2  
S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv anti  
A:Reference number: S41374

A:Accession: S41374  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-249 <ART>  
A:Cross-references: EMBL:z29480

Query Match 35.0%; Score 571.5; DB 2; Length 249;  
Best Local Similarity 48.3%; Pred. No. 3.8e-31;  
Matches 125; Conservative 38; Mismatches 73; Indels 23; Gaps 7;

QY 40 EVOLVGGGVEPESGSLRSCAAGFTDDYCGMSVRAQPGKGLMNGSGTGC 99  
DB 1 QVQLDQSGAEIVRPGASVLTCTASGPNRKYDTHWVKRPEKLEMIARIAPASGVK 60  
QY 100 ADSVKRVTISRDNANKSLYLQMNSLRAEDTAVYCAK--ILGAGRWYFDLNGKGTVA 157  
DB 61 VPRFQKARTITADTSSNTAVYLLSLTSEDTAVYCARPDLTSLGY----WGQSTVA 116  
QY 158 VSSGGGGSGGGGGGGSS-ELTQD-PANVALGQTVRTICQ-----GDSLRSYA 206  
DB 117 VSSRGGGSGGGGGSDIELTQSPSVVYIPGESVISICRSKSLTYSDDGS---YL 172  
QY 207 SWYQKPGQAPVYIVYIGKNRPSGIPDRFSGSSSGMTASLTITGAQAEDEADYCNRSRDS 266  
DB 173 FFWLQRPQSPQLLITRMSVLASGVDRFSGSGSTFTLRISVEADYGVYICMQHRE 232  
QY 267 SGNHVVEGGGKTLTVLGAA 285  
DB 233 --YPLTFGAGTKLEKRAA 249

## RESULT 3

Ig lambda chain V region (clone alpha-B8A3) - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C:Accession: S19663  
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. M.Ol. Biol. 222, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A:Reference number: S19663; MUID:92085276; PMID:1748994  
A:Accession: S19663  
A:Molecule type: mRNA  
A:Residues: 1-109 <MAR>  
A:Cross-references: EMBL:X61640; NID:929492; PIDN:CAA43821.1; PID:91340166  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 568; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.8e-31;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SSELTDPAVSVALGQTVRTICGDSLRSYASWYQKPGQAPVLYYKNNRPSGIPDR 234  
DB 1 SSELTDPAVSVALGQTVRTICGDSLRSYASWYQKPGQAPVLYYKNNRPSGIPDR 60  
QY 235 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVLG 283  
DB 61 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVLG 109

## RESULT 4

Ig lambda chain - human  
S47184  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S47184  
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
Submitted to the EMBL Data Library, June 1994  
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient  
A:Reference number: S47181  
A:Accession: S47184

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <MC1>  
A:Cross-references: EMBL:X79783; NID:9506446; PIDN:CAA56179.1; PID:9506427  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.4%; Score 562; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.9e-31;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SSELTDPAVSVALGQTVRTICGDSLRSYASWYQKPGQAPVLYYKNNRPSGIPDR 234  
DB 1 SSELTDPAVSVALGQTVRTICGDSLRSYASWYQKPGQAPVLYYKNNRPSGIPDR 60  
QY 235 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVL 282  
DB 61 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVL 108

## RESULT 5

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36272  
R:Griffiths, A.D.; Malnqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display library  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36272  
A:Molecule type: mRNA  
A>Status: preliminary; nucleic acid sequence not shown  
A:Accession: S36272  
A:Molecule type: mRNA  
A:Residues: 1-110 <GR1>  
A:Cross-references: EMBL:Z18833; NID:933419; PIDN:CAA79285.1; PID:9939912  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 33.8%; Score 551.5; DB 2; Length 110;  
Best Local Similarity 98.2%; Pred. No. 3.5e-30;  
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 175 SSELTDPAVSVALGQTVRTICGDSLRSYASWYQKPGQAPVLYYKNNRPSGIPDR 234  
DB 1 SSELTDPAVSVALGQTVRTICGDSLRSYASWYQKPGQAPVLYYKNNRPSGIPDR 60  
QY 235 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVLG 283  
DB 61 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVLG 110

## RESULT 6

Ig heavy chain (subclass IgM) - human (fragment)  
S31104  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999  
C:Accession: S31104  
R:Raapport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur Eut. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line VH3 genes and short diverse third comp  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31104  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-121 <RAA>  
A:Cross-references: EMBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>



```
Query Match          33.4%; Score 546; DB 2; Length 121;
Best Local Similarity 84.3%; Pred. No. 9e-30;
Matches 102; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 40 EQVLQSGGVRPRGSLRLSCAASGFTFDYIGASVWVQAQPKGLEWVSGIMWNGSITCY 99
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      1 EQVLQSGGGLVQPKRSRLSCAASGFTFDYAMHWVQAQPKGLEWVSGISWNGSITCY 60
OY 100 ADVVGRVTSRDNKNLSLYLQMSLRADFTAVYVCARKILGAGRGVFPDLMGKGTIVTS 159
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      61 ADVVGRVTSRDNKNLSLYLQMSLRADFTALYICADVFGSGWTFDLMGRGLTVTS 120
OY 160 S 160
      |
      121 S 121
Db

RESULT 7
S70444
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70444; S70426
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70444
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-127 <CUI>
A:Experimental source: clone E29.1
      submitted to the EMBL Data Library, May 1990
A:Reference number: S70426
A:Accession: S70426
A:Molecule type: mRNA
A:Residues: 1-90 <TON>
A:Cross-references: EMBL:X53070
A:Experimental source: cell line E29.1, clone VL 29-1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:1-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F:34-108/Domain: Immunoglobulin homology <IMM>

Query Match          33.4%; Score 546; DB 2; Length 127;
Best Local Similarity 97.2%; Pred. No. 9.4e-30;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 175 SSELQDPAVSAVGQTVRTTCGDSLRSYASWVQAQPKGAQPVLYTYGKNRPSGIPDR 234
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      20 SSELQDPAVSAVGQTVRTTCGDSLRSYASWVQAQPKGAQPVLYTYGKNRPSGIPDR 79
OY 235 FSGSSGNTASLTITGAQAEADADYYCNSRDSSGNHNVFGGKTLTVL 282
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      80 FSGSSGNTASLTITGAQAEADADYYCNSRDSSGNHNVFGGKTLTVL 127
Db

RESULT 8
S38498
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38498
R:Maris, J.D.; Ouwehand, W.H.; Bye, J.M.; Finneern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S
      submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a H
A:Reference number: S38488
A:Accession: S38498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <MAR>
```

```
A:Cross-references: EMBL:Z23035; NID:9414043; PIDN:CAAB0570.1; PID:9414044
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:14-88/Domain: Immunoglobulin homology <IMM>

Query Match          33.1%; Score 541; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.7e-29;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 176 SSELQDPAVSAVGQTVRTTCGDSLRSYASWVQAQPKGAQPVLYTYGKNRPSGIPDR 235
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      1 SSELQDPAVSAVGQTVRTTCGDSLRSYASWVQAQPKGAQPVLYTYGKNRPSGIPDR 60
OY 236 SSGSSGNTASLTITGAQAEADADYYCNSRDSSGNHNVFGGKTLTVL 283
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      61 SSGSSGNTASLTITGAQAEADADYYCNSRDSSGNHNVFGGKTLTVL 108
Db

RESULT 9
S38496
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38496
R:Maris, J.D.; Ouwehand, W.H.; Bye, J.M.; Finneern, R.; Gorlick, B.D.; Voak, D.; Thorpe
      submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38496
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:Z23031; NID:9414039; PIDN:CAAB0566.1; PID:9414040
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-89/Domain: Immunoglobulin homology <IMM>

Query Match          33.0%; Score 539; DB 2; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-29;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 175 SSELQDPAVSAVGQTVRTTCGDSLRSYASWVQAQPKGAQPVLYTYGKNRPSGIPDR 234
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      1 SSELQDPAVSAVGQTVRTTCGDSLRSYASWVQAQPKGAQPVLYTYGKNRPSGIPDR 60
OY 235 FSGSSGNTASLTITGAQAEADADYYCNSRDSSGNHNVFGGKTLTVL 283
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      61 FSGSSGNTASLTITGAQAEADADYYCNSRDSSGNHNVFGGKTLTVL 109
Db

RESULT 10
JC5322
p53 specific single-chain antibody pab421 - human
C:Species: Homo sapiens (man)
C>Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Janot, C.B.; Hynes, N.E.
      Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It resto

Query Match          32.5%; Score 531.5; DB 2; Length 233;
Best Local Similarity 48.0%; Pred. No. 1.6e-28;
Matches 117; Conservative 34; Mismatches 74; Indels 19; Gaps 8;

OY 45 QSGGVRPRGSLRLSCAASGFTFDYIGASVWVQAQPKGLEWVSGIMWNGSITCY 104
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      2 ESGAEIVRSGASVKLSCTTSGFNINDYIMHWVKKRPEQGLEWIGRIDPENGADMTRSSG 61
Db
```

QY	105	GRVITSRPNMAKNSLYLQMSNLSRAEDTAVYYCAKILGAGRGWTFDLMGKTIVTVSSGGG	164
Dd	62	VKATMTAQTSSNTAYLQLSLSTSEDTAVYYC---NAG---MDYWGCGTTVAIVSSGGG	113
QY	165	SGGGSGGGGS-ELTDPPA-VSYALGVVRITCGD---SLRSY-YASYMCOOKPGCAPY	218
Dd	114	SGGRASGGGSDIELTQSPASLAIVLGQATITSCRASKSVSYGYSMHNNQKPGQPPR	173
QY	219	LVIYGKNRPQSIPDRFGSSSGSNFASLTITGAQAEDADAYYC-NSRDSGSHVVGGGT	277
Dd	174	LLIYLVSNLSEGVPARFSGSGSGDTFTLNIIHVFEEDATYYCOQHIRELTRSE---	Ggr 229
QY	278	KLVV 281	
Dd	230	KLEI 233	

```

RESULT 11
S25748
I9_lambdab chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25748
R:Combrato, G.; Kloebeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(Lambda) and J(Lambda)-C(Lambda) gene segments of the human immunoglobulin lambda
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25748
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <CON>
A:Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:148-216/Domain: immunoglobulin homology <IMM>

```

	Query Match	32.5%; Best Local Similarity 91.7%;	Score 530; Pred. No. 2e-28;	DB 2;	Length 233;
	Matches 100;	Conservative 5;	Mismatches 4;	Indels 0;	Gaps 0
QY	175 SSELTPDPAVSVALGQTVTRITCCGSLSYASVSWIQOKGQAPVLVTYCKNNRPPSIPDR				
Db	20 SSELTPDPAVSVALGQTVTRITCCGSLSYASVSWIQOKGQAPVLVTYCKNNRPPSIPDR				
QY	235 FSGSSSGNTASLTITGGADEADADYCCNSRDSGGNHVYFGGCTKTVLG				
Db	80 FSGSSSGNTASLTITGGADEADADYCCNSRDSGGNVHVGCGTCKTVLG				

```

RESULT 12
L3H0SH
Ig lambda chain V-III region (Sh) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C:Accession: A01980
R:Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A:Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete
A:Reference number: A92057; MUID:70166723; PMID:4909564
A:Accession: A01980
A:Molecule type: Protein
A:Residues: 1-108 <TIT>
A:Note: the sequence of the C region is also given
C:Genetics:
A:Gene: GDB:IGLV6
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
;14-88/Domain: immunoglobulin homology <IM>

```

```
F:21-86/Dissulfide bonds: #status experimental
Query Match          32.3%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 1.5e+28;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

OY           176 SELTODPAVSYALCQTVRITCGDSSLNSYYASWFOQRPGCAPVLVIYTGKNNRPSCIPDRF 235  
              |||||  
              |||||  
Db           1 SELTODPAVSVALGQTVRITCGDSSLNGDYDAWFOQRPGCAPVLVIYGRNRRPSPGIDPRF 60  
              |||||

OY           236 SSSSGMNASLITIGAAEDADYYCNCSRSSGHNVFGGGTKLTIVG 283  
              |||||  
Db           61 SGSSSGHNASLITIGAAEDADYYCNCSRSSGHNVLFGGGTKLTLIVG 108  
              |||||

```

RESULT 13
S19672
Ig lambda chain V region (clone alpha-TEU14) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19672
R:Marks: J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Wint
J.: Mol. Biol. 222, 381-357, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on
A:Reference number: S19663; MUID:92085276; PMID:11748994
A:Accession: S19672
A:Molecule type: mRNA
A:Residues: 1-110 <MAR>
A:Cross-references: EMBL:X61644; NID:937856; PIDN:CAA3825.1; PID:g1335384
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:15-89/Domain: immunoglobulin homology <IMM>

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	Query Match	Similarity	31.8%	Score 518.5	DB 2:	length 110;
	Best Local	Similarity	31.8%	Pred. No. 5	5e-28:	
	Matches	101;	Conservative	4;	Mismatches	4;
					Indels	1;
					Gaps	1
QY	175	SSELTQDPAVSYALGQYVRIITCGQSLSSYASYSWQKPGCAPVLYIYKKNRPPSIPDR				234
Db	1	SSELTQDPAVSYALGQYVRIITCGQSLSSYASYSWQKPGCAPVLYIYGENSRPSIPDR				60
QY	235	FSGSSSGNTASLITITGAQAEDEADYVCCNSRDSGGNHV-VFGGGRKLTVLG				283
Db	61	FSGSSSGNTASLITITGAQAEDEADYVCCNSRDSGRHGLEVFGGGRKLTVLG				110

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RESULT 14
S02083
I: lambda chain V-IV region - human (tentative sequence) (fragments)
N: Alternate names: amyloid-fibril protein GIL
C: Species: Homo sapiens (man)
C: Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C: Accession: S02083
R: EYKse, E.M.; Sletten, K.; Husby, G.; Cornwell IIF, G.G.
Biochem. J. 256, 973-980, 1988
A: Title: The primary structure of the variable region of an immunoglobulin IV light-c
A: Reference number: S02083; MUID: 69134210; PMID: 3146981
A: Accession: S02083
A: Molecule type: protein
A: Residues: 1-10;71-72;73-75;76-131;132-146 <EYK>
C: Superfamily: Immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
:14-88/Domain: immunoglobulin homology <IMM>

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Query Match	Similarity	Score	DB 2:	Length	146:
Best Local	91.7%	Pred. No.	8.5e-28:		
Matches	99:	Mismatches	1:	Indels	1:
				Gaps	1:
QY	176	SELTQDPAPVAVSALGTVARITTCQGDLSRSYASVSWYQKQFGQAPLVLYGKNNRPSGIPDRF			235
Db	1	SELTQDPAPVAVSALGTVARITTCQGDLSRNFVSWYQKQFGQAPLVLYGKNNRPSGIPDRF			60
QY	236	SGSSSGNNTASLITTCGAQAEADADYYCNSRDSGN-HVFFGGGKTLLVL			282

Db 61 SSSSGNTASTLTICGARAEDADYCNSSNGVHYFGGFKTLTVL 108

## RESULT 15

S30532

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996

C:Accession: S30532

R:Marlette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30532

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 &lt;MARK&gt;

A:Cross-references: EMBL:Z18318

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F.15-98/Domain: Immunoglobulin homology &lt;IMM&gt;

Query Match 31.2%; Score 509; DB 2; Length 123;

Best Local Similarity 78.9%; Pred. No. 2.6e-27;

Matches 97; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

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OY 40 EVOLVSGGVEPRPGSLRLSCAASGTFEDDYGMWVROAPGKGLEWYSGINMNGSTGY 99
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPERSLRLSCAASGTFEDDYAMHWVROAPGKGLEWVSGISWNSGTLGY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 100 ADSVKGRVTISRDNKNSLYLQMSLRAEDTAVYYCAKILGARGW--YFDLWGKGTVT 157
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFAISRDNKNSLYLQMSLRAEDTALYYCAKDTPTSSGWSNAFDIMWGGMVT 120
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 158 VSS 160
   |||
Db 121 VSS 123
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Search completed: September 22, 2003, 15:14:58  
Job time : 21.9098 secs





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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=75059123; PubMed=4803843;
RX Watanabe S., Barnikol H.U., Horn J., Bettram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H II. Architecture of the complete IgM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN (2)
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC PIR: A02064; M3HUGL.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match
Best Local Similarity 26.8%; Score 437.5; DB 1; Length 116;
Matches 84; Conservative 12; Mismatches 20; Indels 5; Gaps 1;

QY 40 EVQLVDSGGGVPPGSGSLSCAASGFTTDDYGMKVRAPKPKGLEWVGIMNGSTGY 99
DB 1 EVQLVDSGGDLVQPGSLRLSCAASGFTFBPBLGMVTRVAPKPKGLEWVANITZBSGZBY 60
OY 100 ADSVGRVITSRDKNKNSLYLQMSLRARDTAVYVCARKITLGARGVFPDLMKGTIVYS 159
DB 61 VDSVGRFTISRDNKNSLYLQMSLRARDTAVYVCARKITLGARGVFPDLMKGTIVYS 115
OY 160 S 160
DB 116 T 116

RESULT 3
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region BVT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=78137069; PubMed=416441;
RX Torano A., Putnam F.W.;
RA "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT

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RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPIC, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; A2HUBU.
DR HSSP: P01789; 1MCP.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DE52DCFA CRC64;

Query Match
Best Local Similarity 26.7%; Score 436; DB 1; Length 115;
Matches 85; Conservative 18; Mismatches 12; Indels 6; Gaps 2;

QY 40 EVQLVDSGGGVPPGSGSLSCAASGFTTDDYGMKVRAPKPKGLEWVGIMNGSTGY 99
DB 1 EVQLVDSGGDLVQPGSLRLSCAASGFTVBSHSMVTRVAPKPKALZWSAI YRGGTYV 59
OY 100 ADSVGRVITSRDKNKNSLYLQMSLRARDTAVYVCARKITLGARGVFPDLMKGTIVYS 159
DB 60 ADSVGRFTISRDNKNSLYLQMSLRARDTAVYVCARKITLGARGVFPDLMKGTIVYS 114
OY 160 S 160
DB 115 S 115

RESULT 4
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=81101090; PubMed=6450418;
RX Mathysens G., Rabbits T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00236; AA53516.1; -
DR EMBL: M35415; AA58735.1; -
DR PIR: A02047; H3H026.
DR PDB: 1HOU; 23-DEC-99.
DR Genew: HGNC:5545; IGHV@.
DR GO: GO:0005576; C:extracellular; NAS.

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DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 26.3%; Score 429; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 2.6e-24;
Matches 81; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 40 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMGVWRQAPGKGLEWVSGINMGSGTGY 99
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSSYRAMSVWRQAPGKGLEWVSATISGSGSTYY 79

QY 100 ADSVKGAVTISHDNKNSLYLQMSLRAEDTAVVYCAK 137
DB 80 GDSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCAK 117

RESULT 5
HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region H1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE-79124695; PubMed-420800;
RX Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG H1L.";
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02054; G1HJHL.
DR HSSP: P01772; 2F84.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 26.2%; Score 428; DB 1; Length 121;
Best Local Similarity 67.8%; Pred. No. 3.2e-24;
Matches 82; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 40 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMGVWRQAPGKGLEWVSGINMGSGTGY 99
DB 61 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSSYRAMSVWRQAPGKGLEWVSATISGSGSTYY 79
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DB 1 QVKLVQAGGVVQPGGSLRLSCAASGFTFTSSNYGMHVRQAPGKGLEWVAIVYNGSRTYY 60
QY 100 ADSVKGAVTISHDNKNSLYLQMSLRAEDTAVVYCAKLTGARGVFPDLMGKGTTVVS 159
DB 61 GDSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCAKPDILTAFSPDYGQGLVTVVS 120

QY 160 S 160
DB 121 S 121

RESULT 6
HV3U_HUMAN
ID HV3U_HUMAN STANDARD; PRT; 120 AA.
AC P01782;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE-80020921; PubMed-114209;
RX Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT "Amino acid sequence of the heavy-chain variable region of the
RT crystallizable human myeloma protein DOB.";
RL Biochemistry 18:4068-4080(1979).
CC -1- MISCELLANEOUS; THIS GAMMA-1 MYELOMA PROTEIN DOB HAS A HINGE-REGION
CC DELETION.";
RL Biochemistry 18:4054-4067(1979).
CC -1- HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
CC DISULFIDE BONDS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90431; G1HJDB.
DR HSSP: P01772; 2F84.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 26.0%; Score 424.5; DB 1; Length 120;
Best Local Similarity 67.7%; Pred. No. 5.6e-24;
Matches 84; Conservative 10; Mismatches 23; Indels 7; Gaps 2;

QY 40 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMGVWRQAPGKGLEWVSGINMGSGTGY 99
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSSYRAMSVWRQAPGKGLEWVSATISGSGSTYY 79

QY 100 ADSVKGAVTISHDNKNSLYLQMSLRAEDTAVVYCAKLTGARGV---YFDLMGKGTTV 156
DB 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVVYCAK---GYLNGVMWFPDYGQGLTV 116

QY 157 TVSS 160
DB 117 TVSS 120
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RESULT 7
HV3G_HUMAN          STANDARD;          PRT;          122 AA.
ID   HV3G_HUMAN
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE.
RA   MEDLINE=8103859; PubMed=6774332;
RT   Lehman D.W., Putnam F.W.;
RL   "Amino acid sequence of the variable region of a human mu chain:
RL   location of a possible JH segment."
CC   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC   PATIENT WITH MACROGLOBULINEMIA.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR: A02051; M3HUM.
DR   HSSP: P01772; 2FB4.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-Like.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF00047; Ig; 1.
DR   SMART: SM00406; IGV; 1.
DR   PROSITE: PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyridolone carboxylic acid.
FT   DOMAIN          1      112      IG-LIKE.
FT   MOD_RES         1      122      PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER         122      122
SQ   SEQUENCE      122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match      26.0%; Score 424.5; DB 1; Length 122;
Best Local Similarity 66.1%; Pred. No. 5.7e-24;
Matches 82; Conservative 18; Mismatches 19; Indels 5; Gaps 2;

QY   40  EVQLVDSGGVERPGSLRLSCAASGFTPDYGMWVRAAPGKLEWVSGINMGSTGY 99
DB   1  QVELVDSGGGVYVPGSLRLSCAASGFTFSNVMHWVROPKGLWVAVISYBGBKXY 60
QY   100 ADSVKRGVITSRNMAKNSLYLQMSLRADETAVYYCAK---IIAGRGWTFDLMGKTTY 156
DB   61 ADSVKRGFTISRBSKFTLYLQMSLRADETAVYYCAKRDRLPGYRA--FNYWGQGTLY 118
QY   157 TVSS 160
DB   119 TVSS 122

RESULT 8
HV3B_HUMAN          STANDARD;          PRT;          114 AA.
ID   HV3B_HUMAN
AC   P01763;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RX   Gont F., Frangione B.;
```

```
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33."
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC   AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC   WALDENSTROM'S MACROGLOBULINEMIA.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR: A02046; M3HUM.
DR   HSSP: P01772; 2FB4.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-Like.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF00047; Ig; 1.
DR   SMART: SM00406; IGV; 1.
DR   PROSITE: PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyridolone carboxylic acid.
FT   DOMAIN          1      112      IG-LIKE.
FT   MOD_RES         1      114      PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER         114      114
SQ   SEQUENCE      114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match      25.9%; Score 422.5; DB 1; Length 114;
Best Local Similarity 69.4%; Pred. No. 7.4e-24;
Matches 84; Conservative 13; Mismatches 17; Indels 7; Gaps 2;

QY   40  EVQLVDSGGVERPGSLRLSCAASGFTPDYGMWVRAAPGKLEWVSGINMGSTGY 99
DB   1  QVELVDSGGGVYVPGSLRLSCAASGFTFSNVMHWVROPKGLWVAVISYBGBKXY 60
QY   100 ADSVKRGVITSRNMAKNSLYLQMSLRADETAVYYCAKIIAGRGWTFDLMGKTTY 159
DB   61 ADSVKRGFTISRBSKNSLYLQMSLRADETAVYYCA-----KGLNLN-WGQGTLYTS 113
QY   160 S 160
DB   114 S 114

RESULT 9
HV3D_HUMAN          STANDARD;          PRT;          115 AA.
ID   HV3D_HUMAN
AC   P01765;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region TTL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE.
RA   MEDLINE=78005528; PubMed=409716;
RT   Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT   "Immunoglobulin structure and genetics. Identity between variable
RT   regions of a mu and a gamma2 chain."
RL   J. Biol. Chem. 252:7192-7199(1977).
CC   -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC   OF IGM AND IGGB ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC   GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC   IDENTICAL.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR: A02048; H3HUTL.
DR   HSSP: P01772; 2FB4.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-Like.
DR   InterPro: IPR003006; Ig_MHC.
```



DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 108 IG-LIKE.  
 FT NON\_TER 115 115  
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;  
 Query Match 25.7%; Score 419; DB 1; Length 115;  
 Best Local Similarity 68.6%; Pred. No. 1.3e-23;  
 Matches 83; Conservative 12; Mismatches 20; Indels 6; Gaps 2;  
 QY 40 EVOLVQSGGVERPGSLRLSCAASGFTFDDYGMWVQAPGKGLEWVSGINMNGSTGY 99  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYVMSWVQAQCKGLZMWGAIZGLSVSZSY 60  
 QY 100 ADSVKGRTYISRDNAKNSLYLQNMNSLRADPTAVYYCAKILGAGRWYFDLWGKGTYYVS 159  
 DB 61 ABSVKGRTYISRDNSKNTLYLNMNSLRADPTAVYYCAK--GKVSAYYFBYWGZGLTYVVS 114  
 QY 160 S 160  
 DB 115 S 115  
 RESULT 10  
 HV31\_HUMAN STANDARD; PRT; 119 AA.  
 AC P01770;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region NTE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE-77070269; PubMed-826475;  
 RA Ponsingl H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a  
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The  
 RT chymotryptic peptides of the H-chain, alignment of the tryptic  
 RT peptides and discussion of the complete structure.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE-77070267; PubMed-1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA  
 CC PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR: A9168; G1HUNT.  
 DR HSSP: P01772; 2PB4.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT MOD\_RES 1 112 PYROLIIDONE CARBOXYLIC ACID.

FT DISULFID 22 96  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;  
 Query Match 25.3%; Score 413; DB 1; Length 119;  
 Best Local Similarity 66.9%; Pred. No. 3.7e-23;  
 Matches 81; Conservative 15; Mismatches 23; Indels 2; Gaps 1;  
 QY 40 EVOLVQSGGVERPGSLRLSCAASGFTFDDYGMWVQAPGKGLEWVSGINMNGSTGY 99  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYTHWVQAQCKGLEWVAMSYGGBKHY 60  
 QY 100 ADSVKGRTYISRDNAKNSLYLQNMNSLRADPTAVYYCAKILGAGRWYFDLWGKGTYYVS 159  
 DB 61 ADSVKGRTYISRDNSKNTLYLNMNSLRADPTAVYYCAK--RDTAFMHGQGLTYVVS 118  
 QY 160 S 160  
 DB 119 S 119  
 RESULT 11  
 HV01\_CANFA STANDARD; PRT; 114 AA.  
 AC P01784;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region GOM.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE-77242268; PubMed-407924;  
 RA Wasserman R.L., Capra J.D.;  
 RT "Primary structure of the variable regions of two canine  
 RT immunoglobulin heavy chains.";  
 RL Biochemistry 16:3160-3168(1977).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR: A02067; AVDGM.  
 DR HSSP: P01772; 2PB4.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;  
 Query Match 25.3%; Score 412.5; DB 1; Length 114;  
 Best Local Similarity 67.8%; Pred. No. 3.8e-23;  
 Matches 82; Conservative 11; Mismatches 21; Indels 7; Gaps 1;  
 QY 40 EVOLVQSGGVERPGSLRLSCAASGFTFDDYGMWVQAPGKGLEWVSGINMNGSTGY 99  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSGYDMQWVQAQCKGLQKVAFFNDALSAQY 60  
 QY 100 ADSVKGRTYISRDNAKNSLYLQNMNSLRADPTAVYYCAKILGAGRWYFDLWGKGTYYVS 159  
 DB 61 ADAVKGRTYISRDNAKNSLYLQNMNSLRADPTAVYYCAK-----WQFEYWGQGLTYVVS 113  
 QY 160 S 160  
 DB 114 S 114  
 RESULT 12







Result	Score	Query	Match	length	DB	ID	Description
No.							
1	888.5	54.4	298	11	Q9QYF0	Q9QYF0 mus musculi	
2	616	37.7	241	11	Q921A6	Q921A6 mus musculi	
3	552	33.8	107	4	Q9NSD6	Q9NSD6 homo sapien	
4	528	32.3	499	4	Q8NSK4	Q8NSK4 homo sapien	
5	527.5	32.3	112	4	Q9HCC1	Q9HCC1 homo sapien	
6	519.5	31.8	218	11	Q925E1	Q925E1 mus musculi	
7	515.5	31.6	573	4	Q8WU38	Q8WU38 homo sapien	
8	495.5	30.3	471	4	Q8WC77	Q8WC77 homo sapien	
9	473	29.0	121	4	Q9UL71	Q9UL71 homo sapien	
10	468	28.7	613	4	Q8WUK1	Q8WUK1 homo sapien	
11	464.5	28.4	597	4	Q96BB9	Q96BB9 homo sapien	
12	458	28.0	113	4	Q9UL90	Q9UL90 homo sapien	
13	456	27.9	479	11	Q91WP5	Q91WP5 mus musculi	
14	446.5	27.3	487	11	Q99RK4	Q99RK4 mus musculi	
15	442.5	27.1	118	4	Q9UL91	Q9UL91 homo sapien	
16	440	26.9	116	4	Q9UL93	Q9UL93 homo sapien	

17	439.5	26.9	122	4	Q9UL44	Q9UL44 homo sapien
18	435	26.6	473	11	Q9UL65	Q9UL65 mus musculu
19	434	26.6	233	4	Q8TBC9	Q8TBC9 homo sapien
20	427	26.1	104	4	Q9UL87	Q9UL87 homo sapien
21	425.5	26.1	147	4	Q9Y509	Q9Y509 homo sapien
22	425	26.0	493	4	Q8NCL6	Q8NCL6 homo sapien
23	424.5	26.0	494	4	Q96K68	Q96K68 homo sapien
24	423	25.9	480	11	Q91XEL	Q91XEL mus musculu
25	423	25.9	521	4	Q8N4Y9	Q8N4Y9 homo sapien
26	419.5	25.7	118	4	Q9UL72	Q9UL72 homo sapien
27	418	25.7	486	11	Q91U07	Q91U07 mus musculu
28	418	25.6	233	4	Q8N5F4	Q8N5F4 homo sapien
29	410	25.1	119	11	Q92OE7	Q92OE7 mus musculu
30	409	25.0	131	4	Q9UL88	Q9UL88 homo sapien
31	401	24.6	469	11	Q8R3V9	Q8R3V9 mus musculu
32	396.5	24.3	484	11	Q8V2A0	Q8V2A0 mus musculu
33	396	24.2	95	4	Q9ULB6	Q9ULB6 homo sapien
34	384	23.5	170	11	Q925S2	Q925S2 mus musculu
35	381.5	23.4	234	4	Q8N355	Q8N355 homo sapien
36	381	23.3	125	4	Q9UL95	Q9UL95 homo sapien
37	376.5	23.1	124	4	Q9UL92	Q9UL92 homo sapien
38	375	23.0	437	11	Q9R1A4	Q9R1A4 mus musculu
39	371.5	22.7	107	4	Q9UL82	Q9UL82 homo sapien
40	370	22.7	119	4	Q9UL94	Q9UL94 homo sapien
41	366.5	22.4	124	6	Q9N0W4	Q9N0W4 crycitolagus
42	366.5	22.3	124	6	Q9N0M6	Q9N0M6 crycitolagus
43	363.5	22.3	159	4	Q96GS0	Q96GS0 homo sapien
44	363	22.2	237	4	Q9W5X3	Q9W5X3 homo sapien
45	361	22.1	112	4	Q9UGP3	Q9UGP3 homo sapien

## ALIGNMENTS

Q09GYFO	RESULT 1	ID	Q09GYFO	PRELIMINARY;	PRT;	298 AA.
AC	Q09GYFO;	AC	Q09GYFO;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	CN 8 scfV.	DE	CN 8 scfV.			
GN	CN 8.	GN	CN 8.			
OC	Mus musculus (Mouse).	OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;	OX	NCBI_TaxID=10090;			
RN	[1]	RN	[1]			
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.			
RC	STRAIN=balb/c; TISSUE=Spleen;	RC	STRAIN=balb/c; TISSUE=Spleen;			
RX	MEDLINE=20183931; PubMed=10706631;	RX	MEDLINE=20183931; PubMed=10706631;			
RA	Shinobara N., Demura T., Fukuda H.;	RA	Shinobara N., Demura T., Fukuda H.;			
RT	Isolation of a vascular cell wall-specific monoclonal antibody	RT	Isolation of a vascular cell wall-specific monoclonal antibody			
RT	recognizing a cell polarity by using a phase display subtraction	RT	recognizing a cell polarity by using a phase display subtraction			
RT	method.;	RT	method.;			
DR	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).	DR	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).			
DR	EMBL; ABO36341; BAA88633.1; .	DR	EMBL; ABO36341; BAA88633.1; .			
DR	HSSP; P01607; IREI.	DR	HSSP; P01607; IREI.			
DR	InterPro: IPR007110; Ig-like.	DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003006; Ig_MHC.	DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_v.	DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF00047; Ig_2.	DR	Pfam: PF00047; Ig_2.			
DR	SMART; SMO0406; IGV; 2.	DR	SMART; SMO0406; IGV; 2.			
DR	PROSITE; PSS0835; IG_LIKE; 2.	DR	PROSITE; PSS0835; IG_LIKE; 2.			
SO	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;	SO	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;			
QY	Query Match	QY	Query Match			
QY	Best Local Similarity 54.4%; Score 888.5; DB 11; Length 298;	QY	Best Local Similarity 54.4%; Score 888.5; DB 11; Length 298;			
QY	Matches 180; Conservative 29; Mismatches 67; Indels 17; Gaps 5	QY	Matches 180; Conservative 29; Mismatches 67; Indels 17; Gaps 5			
QY	1 MMITPSPCAFFLEIFNNKKLLFAIPLVVPPFAAPAAAEVQLVDSGGGVRRPGSGIARLS 60	QY	1 MMITPSPCAFFLEIFNNKKLLFAIPLVVPPFAAPAAAEVQLVDSGGGVRRPGSGIARLS 60			
QY	1 MMITPSPCAFFLEIFNNKKLLFAIPLVVPPFAAPAAAEVQLVDSGGGVRRPGSGIARLS 60	QY	1 MMITPSPCAFFLEIFNNKKLLFAIPLVVPPFAAPAAAEVQLVDSGGGVRRPGSGIARLS 60			



KA  
SClausberg K.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases  
DR EMBL; BC021276; AAH21276.1; -  
DR InterPro; IPR007110; I9-I10;  
DR InterPro; IPR003006; I9-MHC.  
DR InterPro; IPR003596; I9-V.  
DR Pfam; PF00047; I9; 4.





ID	Q91WP5	PRELIMINARY:	PRF:	479 AA.
AC	Q91WP5;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical 51.6 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_TaxID=10090;			
RP	[1]			
RF	SEQUENCE FROM N.A.			

RC TISSUE-Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC013656; AAH13656.1;  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_4.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 27.9%; Score 456; DB 11; Length 479;  
 Best Local Similarity 45.0%; Pred. No. 2.4e-26;  
 Matches 103; Conservative 25; Mismatches 43; Indels 58; Gaps 5;

QY 23 FAIPLVPPYAAQPAAEVQVLOS GGVERPGSLRLSCAASGFTDDYGMVWVROAPGK 82  
 DB 3 FGLTLFLVLTLLKVOCEVQVLES GGGLVPGSGSLVSCAASGLTFSSYAMVWVROSPER 62  
 QY 83 GLEWVSGIMWNGSGTGYADSVKGRVTISRDNANKNSLYLQWNSLRADTAAYYCAKILGAG 142  
 DB 63 RLEWVAALNSNGCNTYISDTMKRFTISRDNASTLYLQWNSLRSEDTAAYYCV----- 116  
 QY 143 RGVYFDLMKGTIVVS-----SSGSGSGG 168  
 DB 117 RGGYFDVWAGTAVTYSSEPARPTIPLTPQALSSDPYIIICLIHDYFPGSTMNVTWG 176  
 QY 169 GSG-----GGG-----SSELTQDPNAVVALGQTVRTTCGDS 200  
 DB 177 KSGKDTITVNFPPALASGGRYTMSQTLT-PAVECEGESVKSCSVQHD 224

## RESULT 14

Q99KA4 PRELIMINARY; PRT; 487 AA.  
 ID 099KA4;  
 AC 099KA4;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical 52.6 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC004786; AAH04786.1;  
 DR HSSP: P01810; 2FB4.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_4.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 27.3%; Score 446.5; DB 11; Length 487;  
 Best Local Similarity 44.8%; Pred. No. 1.3e-25;  
 Matches 104; Conservative 24; Mismatches 49; Indels 55; Gaps 6;

QY 23 FAIPLVPPYAAQPAAEVQVLOS GGVERPGSLRLSCAASGFTDDYGMVWVROAPGK 82  
 DB 3 FGLTLFLVLTLLKVOCEVQVLES GGGLVPGSGSLRLSCAASGFTSSYAMVWVROTPER 62  
 QY 83 GLEWVSGIMWNGSGTGYADSVKGRVTISRDNANKNSLYLQWNSLRADTAAYYCAKILGAG 142

DB 63 RLEWVATISDGSYTYPDNVAAGFTISRDNANKNSLYLQWNSHLKSEDTAMYYCARDMG 122  
 QY 143 -RGVY--FDLMKGTIVVSSG----- 162  
 DB 123 PYGGYRFPYWGCGTITVSSSARNPPTIPLTPALSSDPYIIICLIHDYFPGSTMN 182  
 QY 163 --GSGG-----GSELTQDPNAVVALGQTVRTTCGDS 200  
 DB 183 TWGKSGKDTITVNFPPALASGGGYTMSQTLT-PAVECEGESVKSCSVQHD 233

## RESULT 15

Q9UL91 PRELIMINARY; PRT; 118 AA.  
 ID Q9UL91;  
 AC Q9UL91;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive Immunoglobulin heavy chain variable region (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035023; AAD56259.1;  
 DR HSSP: P01772; 2FB4.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; IGV\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 118  
 SQ SEQUENCE 118 AA; 12843 MW; D063949F2AC149D CRC64;

Query Match 27.1%; Score 442.5; DB 4; Length 118;  
 Best Local Similarity 74.2%; Pred. No. 4.5e-26;  
 Matches 89; Conservative 9; Mismatches 19; Indels 3; Gaps 1;

QY 40 EVQVLOS GGVERPGSLRLSCAASGFTDDYGMVWVROAPGKLEWVSGIMWNGSGTGY 99  
 DB 1 EVQVLES GGGLVQVPGSGSLRLSCAASGFTSSYAMVWVROAPGKLEWVSISSITITTY 60  
 QY 100 ADSVKGRVTISRDNANKNSLYLQWNSLRADTAAYYCAKILGAGRGVYFDLMKGTIVVS 159  
 DB 61 ADSVKGRFTISRDNANKNSLYLQWNSLRADTAAYYCAR--GDSEAFDIMGQGTIVVS 117

Search completed: September 22, 2003, 15:21:23  
 Job time : 52.449 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 52.2793 Seconds  
(without alignments)  
947.272 Million cell updates/sec

Title: US-10-052-798-10  
Perfect score: 1642  
Sequence: 1 MTMTSPSGAFLEIFNVKK.....HHGAAERKLSEEDLNGAA 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03: \*  
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: \*  
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: \*  
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17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: \*  
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: \*  
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: \*  
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: \*  
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: \*  
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: \*  
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: \*  
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1642	100.0	312	20	AAW83323
2	1642	100.0	312	23	ABB09604
3	1642	100.0	312	24	ABG74385
4	1460.5	88.9	309	20	AAW83322
5	1460.5	88.9	309	23	ABB09603
6	1460.5	88.9	309	24	ABG74384
7	1231	75.0	310	20	AAW83324
8	1231	75.0	310	23	ABB09605
9	1231	75.0	310	24	ABG74386

10	1194	72.7	277	23	ABG91841	Human antibody fra
11	1194	72.7	277	23	ABG92019	Human antibody fra
12	1194	72.7	277	23	ABG78150	Human Fv molecule
13	1194	72.7	277	23	ABG78328	Human Fv molecule
14	1192	72.6	247	23	ABP45459	Human Blys binding
15	1188	72.4	263	23	ABG92024	Antibody protein #
16	1178.5	71.8	260	23	ABG92023	Antibody protein #
17	1176.5	71.7	282	22	AAE02185	PAM1 single chain
18	1162	70.8	251	23	ABP45583	Human Blys binding
19	1149	70.0	249	23	ABP45098	Human Blys binding
20	1149	70.0	251	23	ABP44941	Human Blys binding
21	1142	69.5	251	23	ABP44971	Human Blys binding
22	1141.5	69.5	266	23	ABG92020	Human antibody fra
23	1139.5	69.4	256	23	ABP45178	Human Blys binding
24	1138.5	69.3	248	23	ABP44905	Human Blys binding
25	1134.5	69.1	248	23	ABP44903	Human Blys binding
26	1134	69.0	237	23	ABP46101	Human Blys binding
27	1133.5	69.0	248	23	ABP44824	Human Blys binding
28	1133	69.0	237	23	ABP46028	Human Blys binding
29	1133	69.0	247	23	ABP44913	Human Blys binding
30	1132.5	69.0	248	23	ABP45312	Human Blys binding
31	1132.5	69.0	290	24	ABP55318	pelb/5AR/twrc/6his
32	1127	68.6	247	23	ABP45753	Human Blys binding
33	1125.5	68.5	240	23	ABP45901	Human Blys binding
34	1125.5	68.5	296	23	ABG60637	Immunoglobulin rel
35	1125	68.5	237	23	ABP45995	Human Blys binding
36	1125	68.5	249	23	ABP45713	Human Blys binding
37	1124.5	68.5	252	23	ABP45720	Human Blys binding
38	1124	68.5	243	23	ABP46045	Human Blys binding
39	1123.5	68.4	240	23	ABP46002	Human Blys binding
40	1123.5	68.4	248	23	ABP44902	Human Blys binding
41	1122	68.3	239	23	ABP46024	Human Blys binding
42	1122	68.3	249	23	ABP45714	Human Blys binding
43	1122	68.3	291	23	AAE92022	Single chain antib
44	1120	68.2	291	23	ABG60632	Immunoglobulin rel
45	1119	68.1	239	23	ABP46007	Human Blys binding

ALIGNMENTS

RESULT 1	
AAW83323	Standard; Protein; 312 AA.
AC	AAW83323;
XX	
DT	16-MAR-1999 (first entry)
XX	
DE	Single chain Apo-2 antibody 2066.
XX	
KW	Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW	tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW	TNF cytokine.
XX	
OS	Homo sapiens.
XX	
PN	W09851793-A1.
XX	
PD	19-NOV-1998.
XX	
PF	14-MAY-1998; 98WO-US09704.
XX	
PR	09-FEB-1998; 98US-0020746.
XX	
PI	15-MAY-1997; 97US-0857216.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
DR	WPI; 1999-045228/04.
XX	
DR	N-PSDB; AAV72533.
XX	

Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and produce antibodies to increase or decrease apoptosis

Example 14; Fig 16; 134pp; English.

The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 antibodies may also be used diagnostically e.g. to detect Apo-2 expression in cells/tissues and in Apo-2 purification. The present sequence represents a single chain Apo-2 antibody, designated 20E6.

SQ Sequence 312 AA:

Query Match 100.0%; Score 1642; DB 20; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.6e-101;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTMTSPSGAFLEIFNVKLLFAIPVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
DB 1 MTMTSPSGAFLEIFNVKLLFAIPVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
QY 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
QY 121 OMNSLRADTAVVYCARLDLKVKGSSGMPDPMGKGTIVTVSSGGGSGGGSGGSSSE 180
DB 121 OMNSLRADTAVVYCARLDLKVKGSSGMPDPMGKGTIVTVSSGGGSGGGSGGSSSE 180
QY 181 LTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
DB 181 LTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGKLTLYGAANHNNHNGAAEQ 300
DB 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGKLTLYGAANHNNHNGAAEQ 300
QY 301 KLISEEDLNGAA 312
DB 301 KLISEEDLNGAA 312

```

RESULT 2  
ID ABB09604 standard; Protein: 312 AA.  
AC ABB09604;  
XX  
XX 29-MAY-2002 (first entry)  
XX  
DE Amino acid sequence of single-chain Apo-2 antibody 20E6.  
XX  
KW Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
XX caspase; apoptosis; cancer; antibody.  
OS Bacteriophage.

XX US6342369-B1.  
XX  
XX 29-JAN-2002.  
XX  
XX 14-MAY-1998; 98US-0079029.  
XX  
XX 15-MAY-1997; 97US-046615P.  
XX 09-FEB-1998; 98US-074119P.  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ;  
XX WPI: 2002-224941/28.  
XX N-PSDB; AB41734.  
XX

New nucleic acids encoding an Apo-2 ligand, useful for activating or stimulating apoptosis in cancer cells, thus especially useful in the treatment of cancer, or in enhancing immune-mediated cell death -  
Example 14; Fig 16; 68pp; English.

The present sequence represents a single-chain Apo-2 antibody, designated 20E6, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural sources.

SQ Sequence 312 AA:

Query Match 100.0%; Score 1642; DB 23; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.6e-101;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTMTSPSGAFLEIFNVKLLFAIPVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
DB 1 MTMTSPSGAFLEIFNVKLLFAIPVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
QY 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
QY 121 OMNSLRADTAVVYCARLDLKVKGSSGMPDPMGKGTIVTVSSGGGSGGGSGGSSSE 180
DB 121 OMNSLRADTAVVYCARLDLKVKGSSGMPDPMGKGTIVTVSSGGGSGGGSGGSSSE 180
QY 181 LTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
DB 181 LTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGKLTLYGAANHNNHNGAAEQ 300
DB 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGKLTLYGAANHNNHNGAAEQ 300
QY 301 KLISEEDLNGAA 312
DB 301 KLISEEDLNGAA 312

```

RESULT 3  
ID ABG74385 standard; Protein: 312 AA.  
AC ABG74385;  
XX  
XX ABG74385;

DT 11-APR-2003 (first entry)  
 XX Single chain antibody (scFv) fragment 20E6.  
 DE  
 XX  
 XX  
 KW Apo-2; tumour necrosis factor family: TNFR; gene therapy;  
 KW apoptosis; tissue-specific typing; affinity purification;  
 KW competitive-type receptor binding assay; mouse; 20E6.  
 XX  
 XX Mus sp.  
 OS  
 XX  
 XX US2002150985-A1.  
 PN  
 XX  
 XX 17-OCT-2002.  
 PD  
 XX  
 XX 02-NOV-2001; 2001US-0052798.  
 PF  
 XX  
 XX 15-MAY-1997; 97US-046615P.  
 PR 09-FEB-1998; 98US-074113P.  
 PR 14-MAY-1998; 98US-0079029.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
 PI  
 XX WPI; 2003-198287/19.  
 DR N-PSDB; ABX16408.  
 DR  
 XX  
 XX New Apo-2 polypeptides and polynucleotides, useful for inducing  
 PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in  
 PT quantitative diagnostic assays, or in generating antibodies against  
 PT Apo-2 .  
 PT  
 XX  
 XX Example 14; Fig 16; 64pp; English.  
 PS  
 XX  
 XX The invention describes a novel isolated Apo-2 polypeptide. The Apo-2  
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo  
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control  
 CC against samples containing unknown quantities of Apo-2, in generating  
 CC antibodies, in affinity purification techniques, and in competitive-type  
 CC receptor binding assays when labelled with, for instance, radioiodine,  
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
 CC diagnostic for tissue-specific typing. This is the amino acid sequence  
 CC of the single chain antibody fragment (scFv) 20E6 used in the  
 CC preparation of anti-apo-2 antibodies.  
 CC  
 XX  
 XX Sequence 312 AA;  
 SQ  
 Query Match 100.0%; Score 1642; DB 24; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-101;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTTSPFGAFLEIFNVKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVOPGSLRLS 60  
 DB 1 MTMTTSPFGAFLEIFNVKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVOPGSLRLS 60  
 QY 61 CAASGFTSSYWMWSWVQADPKLEWVANIKODSEKRYVDSVYGRFTTISDNKNSLYL 120  
 DB 61 CAASGFTSSYWMWSWVQADPKLEWVANIKODSEKRYVDSVYGRFTTISDNKNSLYL 120  
 QY 121 QMNSLRADPTAVYYCANDLLKVGSSSGFTDPMGRGTTVVYSSGGSGSGSGSGSSSE 180  
 DB 121 QMNSLRADPTAVYYCANDLLKVGSSSGFTDPMGRGTTVVYSSGGSGSGSGSGSSSE 180  
 QY 181 LTQDDPAVSVALGQVTRITCGDSLRSYYASMYOQKPCQDAVLVLYGKNNRPSGIPDRFSG 240  
 DB 181 LTQDDPAVSVALGQVTRITCGDSLRSYYASMYOQKPCQDAVLVLYGKNNRPSGIPDRFSG 240  
 QY 241 SSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGKTLVTLGAANHHNHHGADEQ 300  
 DB 241 SSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGKTLVTLGAANHHNHHGADEQ 300  
 QY 301 KLISEEDLNGAA 312  
 DB 301 KLISEEDLNGAA 312

DB 301 KLISEEDLNGAA 312  
 RESULT 4  
 ID AAW83322  
 AC AAW83322 standard; Protein; 309 AA.  
 XX  
 XX AAW83322;  
 AC  
 XX  
 XX 16-MAR-1999 (first entry)  
 DT  
 XX  
 XX Single chain Apo-2 antibody 16E2.  
 DE  
 XX  
 XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
 KW TNF cytokine.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9851793-A1.  
 PN  
 XX  
 XX 19-NOV-1998.  
 PD  
 XX  
 XX 14-MAY-1998; 98WO-US09704.  
 PF  
 XX  
 XX 09-FEB-1998; 98US-0020746.  
 PR 15-MAY-1997; 97US-0857216.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
 PI  
 XX WPI; 1999-045228/04.  
 DR N-PSDB; AAV72532.  
 DR  
 XX  
 XX Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis  
 PT  
 XX  
 XX Example 14; Fig 16; 134pp; English.  
 PS  
 XX  
 XX The present invention describes human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). A agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification. The present  
 CC sequence represents a single chain Apo-2 antibody, designated 16E2.  
 CC  
 XX  
 XX Sequence 309 AA;  
 SQ  
 Query Match 88.9%; Score 1460.5; DB 20; Length 309;  
 Best Local Similarity 90.1%; Pred. No. 1.9e-89;  
 Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTTSPFGAFLEIFNVKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVOPGSLRLS 60  
 DB 1 MTMTTSPFGAFLEIFNVKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVOPGSLRLS 60

OY	61	CAASFTTSSXWMSVWRAPGKGLBMAVINIKODSEKRYVDYSVKGFETTSRDNAKNSLYL	120
Dd	61	CAASFTTDDIGMSVWRAPGKGLEMBYSSIMNNGSGTGADSVKGNVTISRDNAKNSLYL	120
OY	121	QMSLRADTAVYYCARDLLKYKGSSSGN-FDPWGRTTVTVSSGGGSGGGSGGGSSS	179
Dd	121	QMSLRADTAVYYCA---KLFGAGRGMYFDLMCGKTTFVSSGGGSGGGSGGGSSS	167
OY	180	ELTDPPAVALGCVRLTCOGDSLRSYYASMYOQKPGCAPYLITGKNRRPGLIDRFS	239
Dd	177	ELTDPPAVALAGCVRLTCOGDLSLSTYASMTQKPGCAPVLVITGKNRRPGLIDRFS	236
OY	240	GSSSGNTASLTITGAODEADYDCNSRPDSGNHVFFGGCTKLTVLGAANHNNHNGAAE	299
Dd	237	GSSSGNTASLTITGAODEADYDCNSRPDSGNHVFFGGCTKLTVLGAANHNNHNGAAE	266
OY	300	OKLISEEDLNGAA	312
Dd	297	OKLISEEDLNGAA	309

RESULT	5
ABB09603	
ID	ABB09603 standard; Protein; 309 AA.
XX	
AC	ABB09603;
XX	
DT	29-MAY-2002 (first entry)
XX	
DE	Amino acid sequence of single-chain Apo-2 antibody 16E2

KW Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
 RV caspase; apoptosis; cancer; antibody.  
 XX  
 OS Bacteriophage.  
 XX  
 PN US6342369-B1.  
 XX  
 XX  
 PD 29-JAN-2002.  
 XX  
 XX  
 PE 14-MAY-1998; 98US-0079029.  
 XX  
 XX 15-MAY-1997; 97US-046615P.  
 PR 09-FEB-1998; 98US-074119P.  
 XX  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX  
 PI Ashkenazi AJ;  
 XX  
 DR WPI: 2002-224941/28.  
 N-PSDB; ABL41733.  
 XX  
 XX  
 PT New nucleic acids encoding an Apo-2 ligand, useful for activating or  
 PT stimulating apoptosis in cancer cells, thus especially useful in the  
 PT treatment of cancer, or in enhancing immune-mediated cell death  
 XX  
 ES Example 14; Fig 16; 68pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated  
CC 16E2, which is isolated from a phage library. It is believed that  
CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)  
CC family. Apo-2 polypeptide is capable of triggering caspase-dependent  
CC apoptosis and activating nuclear factor-kappa B. A soluble  
CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2  
CC antibodies may be used to activate or stimulate apoptosis in cancer  
CC cells. They are therefore especially useful in the treatment of cancer,  
CC to enhance immune-mediated cell death in cells expressing Apo-2, to  
CC detect expression of Apo-2 in specific cells, tissues or serum, and in  
CC affinity purification of Apo-2 from recombinant cell culture or natural  
CC sources.

Query Match	88.9%;	Score 1460.5;	DB 23;	Length 309;
Best Local Similarity	90.1%;	Pred. No. 1.9e-89;		
Matches 282;	Conservative	8;	Mismatches 18;	Indels 5;
				Gaps 2

QY	1	MMITPFSFGAFLEITFNVKLLFLAIPLVPPFAAPAAAGVOLVSGGGGLVOPGSGURLS	60
Db	1	MMITPFSFGAFLEITFNVKLLFLAIPLVPPFAAPAAAEVOLVSGGGVERPBGSGURLS	60
QY	61	CAASGTFSSYWMYSWVROAPRGKGLMEVANIKODGSEKYYVDVSKGRFTISHDNKNSLYL	120
Db	61	CAASGTFPDDYCGMSWVROAPRGKGLEWVSGIMNNGSGTGADSVAGRTYISHDNKNSLYL	120
QY	121	QMSLRAEDPTAVYYCARDLLKYKGGSSGN-FDPMGRGTTVYSSGGGGSGGGSGGGSS	179
Db	121	QMSLRAEDPTAVYYCA---KILGARGWYFDLMCKGTTVYSSGGGGSGGGSGGGSS	176
QY	180	ELTQDPAVSYALGQVYRITCGDSLRYTASYAQKPCQAPVLVLYGKNNRPSGIPRFS	239
Db	177	ELTQDPAVSYALGQVYRITCGDSLRYTASYAQKPCQAPVLVLYGKNNRPSGIPRFS	236
QY	240	GSSSGGMTASTTTCGADEDEADYTCNSRDSGNHYVPEGGRKTLVGAANHHNHGAAE	299
Db	237	GSSSGGMTASTTTCGADEDEADYTCNSRDSGNHYVFGGRTKLVGAANHHNHGAAE	296
QY	300	QKLTSEEDLNGAA	312
Db	297	QKLTSEEDLNGAA	309

RESULT 6	
ABG74384	
ID	ABG74384 standard; Protein: 309 AA.
XX	
AC	ABG74384;
XX	
DT	11-APR-2003 (first entry)
XX	
DE	Single chain antibody (scFv) fragment 16E2.
XX	
KM	Apo-2: tumour necrosis factor family; TNF; gene therapy;
KM	apoptosis; tissue-specific typing; affinity purification;
KM	competitive-type receptor binding assay; mouse; 16E2.
XX	
OS	Mus sp.
XX	
PN	US2002150985-A1.
XX	
PD	17-OCT-2002.
XX	
PF	02-NOV-2001; 2001US-0052798.
XX	
PR	15-MAY-1997; 97US-046615P.
PR	09-FEB-1998; 98US-074119P.
PR	14-MAY-1998; 98US-0079029.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX	
DR	WPI: 2003-198287/19.
DR	N-PSDB; ABX16407.
XX	
PT	New Apo-2 polypeptides and polynucleotides, useful for inducing
PT	apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
PT	quantitative diagnostic assays, or in generating antibodies against
PT	Apo-2 -
XX	
PS	Example 14; Fig 16; 64pp; English.
XX	
CC	The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
CC	polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
CC	or ex vivo gene therapy, in quantitative diagnostic assays, as a control
CC	against samples containing unknown quantities of Apo-2, in generating

CC antibodies, in affinity purification techniques, and in competitive-type  
CC receptor binding assays when labelled with, for instance, radiiodine,  
CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
CC diagnostic for tissue-specific typing. This is the amino acid sequence  
CC of the single chain antibody fragment (scFv) 16E2 used in the  
CC preparation of anti-apo-2 antibodies.

XX Sequence 309 AA;

Query Match 88.9%; Score 1460.5; DB 24; Length 309;  
Best Local Similarity 90.1%; Pred. No. 1.9e-89;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPPFYAOPAMAGVOLVESGGGLVPGSGRLS 60  
D 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPPFYAOPAMAEQVLQVSGGVYRPGSGRLS 60  
QY 61 CAASGFFPSSYWMVQAPKGLVWVANTIKDGSERYVDSVKGRTTISRDNKNSLYL 120  
D 61 CAASGFFPDDYGMVWVQAPKGLVWVSGIWMNGSGTYADSVKGRVYISRDNKNSLYL 120  
QY 121 OMNSLRADPVAHYVCARDLKVKGSSSGW-FDPWGRGTPTVYSSGGSGSGSGSGSS 179  
D 121 OMNSLRADPVAHYICA---KILGAGRWTFDLWGKGTIVYSSGGSGSGSGSGSS 176  
QY 180 ELTODPAVSVALGOTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPRFS 239  
D 177 ELTODPAVSVALGOTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPRFS 236  
QY 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFGGKTLYLGAHHHHHGA 299  
D 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFGGKTLYLGAHHHHHGA 296  
QY 300 OKLISEEDLNGAA 312  
D 297 OKLISEEDLNGAA 309

RESULT 7

AAW83324  
ID AAW83324 standard; Protein: 310 AA.

AC AAW83324;

XX 16-MAR-1999 (first entry)

XX Single chain Apo-2 antibody 24C4.

XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
XX TNF cytokine.

XX Homo sapiens.

XX MO9851793-A1.

XX 19-NOV-1998.

XX 14-MAY-1998; 98WO-US09704.

XX 09-FEB-1998; 98US-0020746.

XX 15-MAY-1997; 97US-0857216.

XX (GERTH) GENENTECH INC.

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KU;

XX WPI; 1999-045228/04.

XX N-PSDB: AAV72534.

XX Human Apo-2 polypeptide inducing apoptosis - useful to treat  
PT conditions linked with decreased apoptosis e.g. cancer, and produce  
PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

XX The present invention describes human Apo-2. Apo-2 can be used  
PS therapeutically to induce apoptosis in mammalian cells, and so is useful  
XX to treat conditions associated with decreased apoptosis e.g. cancer.  
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
CC can be used to identify agents activating Apo-2, useful to treat  
CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
CC therapeutically (e.g. those containing immunoglobulin sequences can be  
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
CC antibodies). It can be used to produce antibodies which can be combined  
CC with a (particularly pharmaceutically acceptable) carrier in compositions  
CC or used to produce dimeric molecules (especially homodimeric molecules  
CC comprising first and second Apo-2 antibodies). Agonistic (especially  
CC single-chain) antibodies can be administered to induce apoptosis in  
CC mammalian cancer cells, and antagonistic antibodies used to block  
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
CC antibodies may also be used diagnostically e.g. to detect Apo-2  
CC expression in cells/tissues and in Apo-2 purification. The present  
CC sequence represents a single chain Apo-2 antibody, designated 24C4.

XX Sequence 310 AA;

Query Match 75.0%; Score 1231; DB 20; Length 310;  
Best Local Similarity 77.7%; Pred. No. 3.3e-74;  
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPPFYAOPAMAGVOLVESGGGLVPGSGRLS 60  
D 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPPFYAOPAMAEQVLQVSGGVYRPGSGRLS 60  
QY 61 CAASGFFPSSYWMVQAPKGLVWVANTIKDGSERYVDSVKGRTTISRDNKNSLYL 120  
D 61 CAASGFFPSSYGMVWVQAPKGLVWVAGIFPDGKNKYADSVKGRFTISRDNKNSLYL 120  
QY 121 OMNSLRADPVAHYVCARDLKVKGSSSGW-FDPWGRGTPTVYSSGGSGSGSGSGSS 178  
D 121 OMNSLRADPVAHYCARD-----RGYYMDWVGKGTIVYSSGGSGSGSGSGSS 172  
QY 179 -SELTODPAVSVALGOTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGI 234  
D 173 QSVLTQPPSVSAGAGQRYTISCTGRSSNIGAGHYHMYQQLPGAPKILLITDSDNRPSGV 232  
QY 235 PDRESGSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFGGKTLYLGAHHHHH 294  
D 233 PDRESGSGSNTASLTITGAQAEDEADYYCNSRDSGNSVFGGKTLYLGAHHHHH 292  
QY 295 HGAAEOKLISEEDLNGAA 312  
D 293 HGAAEOKLISEEDLNGAA 310

RESULT 8

ABB09605  
ID ABB09605 standard; Protein: 310 AA.

XX ABB09605;

XX 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 24C4.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
KW caspase; apoptosis; cancer; antibody.

XX Bacteriophage.

XX US6342369-B1.

```
PD 29-JAN-2002.
XX PF 14-MAY-1998; 98US-0079029.
XX PR 15-MAY-1997; 97US-046615P.
XX PR 09-FEB-1998; 98US-074119P.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ;
XX DR WPI: 2002-224941/28.
XX DR N-PSDB; ABL41735.
XX PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
XX PR stimulating apoptosis in cancer cells, thus especially useful in the
XX PR treatment of cancer, or in enhancing immune-mediated cell death
XX PS Example 14; Fig 16; 68pp; English.
XX XX
XX CC The present sequence represents a single-chain Apo-2 antibody, designated
XX CC 24C4, which is isolated from a phage library. It is believed that
XX CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
XX CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
XX CC apoptosis and activating nuclear factor-kappa B. A soluble
XX CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
XX CC antibodies may be used to activate or stimulate apoptosis in cancer
XX CC cells. They are therefore especially useful in the treatment of cancer,
XX CC to enhance immune-mediated cell death in cells expressing Apo-2, to
XX CC detect expression of Apo-2 in specific cells, tissues or serum, and in
XX CC affinity purification of Apo-2 from recombinant cell culture or natural
XX CC sources.
XX SQ Sequence 310 AA;
XX
XX Query Match 75.0%; Score 1231; DB 23; Length 310;
XX Best Local Similarity 77.7%; Pred. No. 3.3e-74;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
OY 1 MTMTSPSGAFLEIFNVKLLFAIPLVVFFYAAQPMAGVOLVSGGGLVOPGSLRLS 60
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVVFFYAAQPMAGVOLVSGGGLVOPGSLRLS 60
OY 61 CAASGFTSSYWMVSWROAPGKGLFEMVANI KODGSEKTYVDSVKRFTISRDNANSLYL 120
DB 61 CAASGFTSSYGMHVRQAPGKGLFEMVAGIFDGNKTYADSVKRFITSRDNSKNTLYL 120
OY 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
DB 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
OY 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
DB 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
OY 179 -SELTQDPAYVALGQTVRITCOGDSLR---SYVASWYQOKPGQAPVLYTIGKNNRPSGI 234
DB 173 QSVLTQPPSVSGAPQORVYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLITDDSNRPSGV 232
OY 235 PDRFSGSSSGNTASLTITGAQAEADADYCNRSDDSGNNHVVFGGCTKTLVLGAANHHNH 294
DB 233 PDRFSGSSSGNTASLTITGAQAEADADYCNRSDDSGNNHVVFGGCTKTLVLGAANHHNH 292
OY 295 HGAEOKLISEEDLNGAA 312
DB 293 HGAEOKLISEEDLNGAA 310
XX
XX RESULT 9
XX ABG74386
XX ID ABG74386 standard: Protein; 310 AA.
XX AC ABG74386;
XX AC
XX AC
XX DT 11-APR-2003 (first entry)
XX XX
XX Single chain antibody (scfv) fragment 24C4.
```

```
XX XX
XX KW Apo-2; tumour necrosis factor family; TNFR; gene therapy;
XX KW apoptosis; tissue-specific typing; affinity purification;
XX KW competitive-type receptor binding assay; mouse; 24C4.
XX OS Mus sp.
XX PN US2002150985-A1.
XX XX
XX PD 17-OCT-2002.
XX XX
XX PF 02-NOV-2001; 2001US-0052798.
XX XX
XX PR 15-MAY-1997; 97US-046615P.
XX PR 09-FEB-1998; 98US-074119P.
XX PR 14-MAY-1998; 98US-0079029.
XX XX
XX PA (GETH ) GENENTECH INC.
XX PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX DR WPI: 2003-198287/19.
XX DR N-PSDB; ABX16409.
XX XX
XX PT New Apo-2 polypeptides and polynucleotides, useful for inducing
XX PR apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
XX PR quantitative diagnostic assays, or in generating antibodies against
XX PR Apo-2.
XX PS Example 14; Fig 16; 64pp; English.
XX XX
XX CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
XX CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
XX CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
XX CC against samples containing unknown quantities of Apo-2, in generating
XX CC antibodies, in affinity purification techniques, and in competitive-type
XX CC receptor binding assays when labelled with, for instance, radiolabel,
XX CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
XX CC diagnostic for tissue-specific typing. This is the amino acid sequence
XX CC of the single chain antibody fragment (scfv) 24C4 used in the
XX CC preparation of anti-apo-2 antibodies.
XX SQ Sequence 310 AA;
XX
XX Query Match 75.0%; Score 1231; DB 24; Length 310;
XX Best Local Similarity 77.7%; Pred. No. 3.3e-74;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
OY 1 MTMTSPSGAFLEIFNVKLLFAIPLVVFFYAAQPMAGVOLVSGGGLVOPGSLRLS 60
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVVFFYAAQPMAGVOLVSGGGLVOPGSLRLS 60
OY 61 CAASGFTSSYWMVSWROAPGKGLFEMVANI KODGSEKTYVDSVKRFTISRDNANSLYL 120
DB 61 CAASGFTSSYGMHVRQAPGKGLFEMVAGIFDGNKTYADSVKRFITSRDNSKNTLYL 120
OY 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
DB 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
OY 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
DB 121 QMNSLRADDTAVYYCARDLKYKSSSGWF--DPWGRGTYYTVVSSGGSGSGGSGGGS 178
OY 179 -SELTQDPAYVALGQTVRITCOGDSLR---SYVASWYQOKPGQAPVLYTIGKNNRPSGI 234
DB 173 QSVLTQPPSVSGAPQORVYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLITDDSNRPSGV 232
OY 235 PDRFSGSSSGNTASLTITGAQAEADADYCNRSDDSGNNHVVFGGCTKTLVLGAANHHNH 294
DB 233 PDRFSGSSSGNTASLTITGAQAEADADYCNRSDDSGNNHVVFGGCTKTLVLGAANHHNH 292
OY 295 HGAEOKLISEEDLNGAA 312
DB 293 HGAEOKLISEEDLNGAA 310
```



RESULT 10  
ABG91841  
ID ABG91841 standard; Protein: 277 AA.  
XX  
XX  
AC ABG91841;  
XX  
XX  
DT 04-DEC-2002 (first entry)  
XX  
XX  
DE Human antibody fragment #25.  
XX  
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
metastasis; hypervariable region; autoimmune disease; thrombosis;  
restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
myocardial infarction; relinopathic disease; abnormal platelet function;  
suphalated tyrosine-dependent protein-protein interaction.

Qy	93	DSEEEKYVDSVKGRFTISDNANKSLYLQMNSLRAEDTAVYCYCARDLKYKGGSSGWFDP	152
Db	76	NGSSTGYADSVKRFETISDNANKSLNYLQMNSLRAEDTAVYCYCARMAPV-----I	126
Qy	153	WGRGTIVTVSSGGGGGGGGSGGGSSSELTODPAVVALGOTVAITTCGGSLRYSWSW	212
Db	127	WGGGTLTVYSSRGGGGSGGGSGGGSSSELTODPAVVALGOTVAITTCGGSLRYSWSW	186
Qy	213	QQRPGQAPVLYITGKNNRPSGIPDRFSSGSSGNTASLTITGAQADEADYCYNSRDSG	272
Db	187	QQRPGQAPVLYITGKNNRPSGIPDRFSSGSSGNTASLTITGAQADEADYCYNSRDSG	246
Qy	273	HVYFEGGKTLTVLGAANHHHHHGAEOKLISEEDLNGAA	312
Db	247	HVYFEGGKTLTVLGA-----AAEOKLISEEDLNGAA	277

WO200253700-A2.

11-JUL-2002.

31-DEC-2001; 2001WO-US49442.

29-DEC-2000; 2000US-258948P.

29-DEC-2000; 2000US-0751181.

(BIOT-) BIO-TECHNOLOGY GEN CORP.

Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H; Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A; WPI: 2002-674776/72.

Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer

Claim 23; Page 233-234; 310pp; English.

The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention.

XX	RESULT 11
XX	ABG92019
XX	ID ABG92019 standard; Protein; 277 AA.
XX	AC
XX	ABG92019;
XX	DT
XX	04-DEC-2002 (first entry)
XX	DE
XX	Human antibody fragment #203.
XX	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX	KW metastasis; hyperariable region; autoimmune disease; thrombosis;
XX	KW retenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX	KW myocardial infarction; retinophthc disease; abnormal platelet function;
XX	KW suplated tyrosine-dependent protein-protein interaction.
XX	OS Homo sapiens.
XX	PN MO200253700-A2.
XX	PD 11-JUL-2002.
XX	PF 31-DEC-2001; 2001MO-US49442.
XX	PR 29-DEC-2000; 2000OUS-258948P.
XX	PR 29-DEC-2000; 2000OUS-0751181.
XX	PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX	P1 Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX	P1 Sznaton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX	DR WPI; 2002-674776/72.
XX	PT
XX	PT Novel isolated epitope present on cancer cells and important in
XX	PT physiological phenomena such as cell rolling, metastasis and
XX	PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX	PT diseases, and cancer -
XX	PS
XX	PS Claim 23; Page 308-309; 310pp; English.
XX	CC
XX	CC The invention relates to an isolated epitope present on cancer cells and
XX	CC important in physiological phenomena such as cell rolling, metastasis and
XX	CC inflammation, where the epitope is capable of being bound by an antibody,
XX	CC its antigen-binding fragment or its complex comprising at least one
XX	CC

	Query Match	72.7%	Score 1194:	DB 23:	Length 277:
	Best Local Similarity	85.0%:	Pred. No. 8,5e-72:		
	Matches 236:	Conservative 5:	Mismatches 12:	Indels 18:	Gaps 2
Oy	33	AAOPAMAGVOLVESGGGLVDPGGSRLRLSCASGFFTSYWMSSWVAQDAGKGLEWANI	KO	92	
Db	16	AAOPAMAEVOLVESGGGVYRRPGSRLRLSCASGFFFDYGMSSWVAQDAGKGLEWNGI	NW	75	

CC or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and

treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention.

**SQ Sequence 277 AA;**

Query Match	72.7%	Score 1194;	DB 23;	Length 277;
Best Local Similarity	85.0%	Pred. No. 8.5e-72;		
Matches 238; Conservative	7;	Mismatches 17;	Indels 18;	Gaps 3;

QY	33	AAOPMAVQVLESGGGVLOPGGSLPLSCAASGFTSSYWMSSVRAQAPGKGLEWMANIKQ	92
Db	16	AAOPMAEVLQLESGGGVVRPGGSLPLSCAASGFTDDGMSVVRQAPGKGLEWGSITNW	75
QY	93	DGSEKYYVDSVKGRETTISRDNAKNSLYLQMSLSRAEDTAVYYCARLLKKKSGSGFDP	152
		:	:
		:	:
Db	76	NGSGTGYADSVKGRETTISRDNAKNSLYLQMSLSRAEDTAVYYCAR-----LTHPYF--	126
QY	153	MGRGTYTVSSSGGGSGGGSGGGSSSELTQPPAVSVALGQYRTTCGGDSLFSYASWY	212
Db	127	WGQGLTVTVSRGGSGGGSGGGSGGGSELTQPPAVSVALGQYRTTCGGDSLFSYASWY	186
QY	213	QOKPQADLVLYYIGKNNRPSGIPDRFSSGSSGCTASTLTITGAQAEDEADYYCNSRPSGN	272
Db	187	QOKPQADPLVLYYIGKNNRPSGIPDRSSGSSGCTASTLTITGAQAEDEADYYCNSRPSGN	246
QY	273	HVYFGGGRKTVLVLGAHHHHHGAAEQKLISEEDLNGAA	312
Db	247	HVYFGGGRKTVLVLGA-----AAEQKLISEEDLNGAA	277

RESULT 12  
ABG78150

ID ABG78150 standard; Protein; 277 AA.

AC ABG78150;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

KW Human; Fv molecule; hypervariable region; single chain Fv; cytosolatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia;  
 KW Lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX  
 OS Homo sapiens.

05 Homo sapiens.

PN W0200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US49440

PR 29-DEC-2000; 2000US-0751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

PI Plaksin D, Peretz T

DR WPI: 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct PT or fragment, or construct of fragment with enhanced binding PT characteristics so as to selectively bind target cell in favour of other

PS Claim 4; Page 155-156; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv

CC molecule a construct or fragments of a construct with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scfv) or a disulfide Fv (dsfv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention.

SQ Sequence 277 AA;

Query Match	72.7%	Score 1194	DB 23	Length 277
Best Local Similarity	85.0%	Pred. No. 8.5e-72		
Matches 238; Conservative	5	Mismatches 19	Indels 18	Gaps 2

QY	33	AAAPRMACVQVLYESGGGGLYOPGGSLRLSCAAAGFFSSYWMSSVRAPECKGLEWVNIQ	92
Db	16	AAQPMALAEQVLESSEGGVVRPGGSLRLSCAAAGFFDDIGMSVRAAPGGLBWSGIMN	75
QY	93	DGESEKYVDVSVKGFETISRDNKAKNSLYLQMSLRDETVAVYVCARDLLKVKSSSGWFPD	152
Db	76	NGSGTYADSVKGFETISRDNKAKNSLYLQMSLRDETVAVYVCARMAPV-----I	126
QY	153	WGRGTTVYVSSGGGGSGGGSGGGSSSELTQPPAYSVALGQVYRITCOGDSLRSYASWY	212
Db	127	WGQGLTVYVSRGGGGSGGGSGGGSSSELTQPPAYSVALGQVYRITCOGDSLSRYASWY	186
QY	213	QOKPCQAEPLVYVGRNNRPSGIPDRFFSGSSSGCNTASLTITGAQAEDEADYCYCSRDSGN	272
Db	187	QOKPCQAEPLVYVGRNNRPSGIPDRSSGSSCNTASLTITGAQAEDEADYCYCSRDSGN	246
QY	273	HVYEGGKTKLYLVGAHHHHHNGAAEQKLISEEDLNGAA	312
Db	247	HVYFGGKTKLYLVGA-----AAEQKLISEEDLNGAA	277

## RESULT 13

ID	ABG78328	standard; Protein; 277 AA.

AC ABG783284

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #203.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
KM lymphoma; myeloma; blastoma; seminoma; acute myeloid leukaemia.

OS Homo sapiens.

PN W0200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US49440

PR 29-DEC-2000; 2000US-0751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A,  
PI Plaksin D, Peretz T;

PI Plaksin D, Peretz T;

DR WPI; 2002-619166/66.

DR N-PSDB; ABS63384.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favour of other  
PT cells -  
XX  
XX  
PS Claim 141; Fig 14; 232pp; English.  
XX  
CC The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention.  
XX  
XX Sequence 277 AA;  
SQ  
Query Match 72.7%; Score 1194; DB 23; Length 277;  
Best Local Similarity 85.0%; Pred. No. 8.5e-72;  
Matches 228; Conservative 7; Mismatches 17; Indels 18; Gaps 3;  
QY 33 AAQPMAGVOLVESGGGLVOPGGSLRLSCAASGFTFSYWMVSWRQAPGKLEWVANIKQ 92  
Db 16 AAQPMAGVOLVESGGGVVPRGSGSLRLSCAASGFTFDDYGMVSWRQAPGKLEWVGINN 75  
QY 93 DSEKTYVDSVKRRFTISRDNANKSLYLQNNSLRAEDTAVYYCARDLLKKGSSGWFDP 152  
Db 76 NGSTGYADSVKRRFTISRDNANKSLYLQNNSLRAEDTAVYYCAR-----LTHPF-- 126  
QY 153 WGRGTYVTYSSGGGSGGGGSSSELTQDPAVSVALLGQTVRITCGDLSRYASWY 212  
Db 127 WGGTLVTVYSRGGGSGGGGSSSELTQDPAVSVALLGQTVRITCGDLSRYASWY 186  
QY 213 QQRPGAPVLYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN 272  
Db 187 QQRPGAPVLYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN 246  
QY 273 HVFVGGGKRLTVLGAHHHHHHHGAADQKLISEEDLNGAA 312  
Db 247 HVFVGGGKRLTVLGA-----AAEQKLISEEDLNGAA 277

RESULT 14  
ABP45459 standard; Protein: 247 AA.  
XX  
XX AC ABP45459;  
XX  
XX DT 19-AUG-2002 (first entry)  
XX  
XX DE Human Bly5 binding scFv SEQ ID 1470.  
XX  
XX KW Bly5; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antithematic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200202641-A1.  
XX  
XX PD 10-JAN-2002.

XX  
XX PF 15-JUN-2001; 2001WO-US19110.  
XX  
XX PR 16-JUN-2000; 2000US-212210P.  
XX PR 17-OCT-2000; 2000US-240816P.  
XX PR 16-MAR-2001; 2001US-276248P.  
XX PR 21-MAR-2001; 2001US-277379P.  
XX PR 25-MAY-2001; 2001US-293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ribben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPL; 2002-114799/15.  
XX  
XX DR Antbodies against B Lymphocyte Stimulating polypeptides, useful for  
XX PT the diagnosis and treatment of cancers and immune disorders -  
XX PS Claim 1; Page 2157-2158; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B Lymphocyte Stimulator (Bly5) polypeptides. Bly5 is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antithematic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Bly5. The antibodies bind to Bly5  
XX and so may be used to detect and quantitate the presence of Bly5 in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Bly5. They may also be  
XX administered to treat diseases associated with aberrant Bly5 expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
XX the antibodies and fragments of the antibodies described in the method  
XX of the invention.  
XX  
XX SQ Sequence 247 AA;  
Query Match 72.6%; Score 1192; DB 23; Length 247;  
Best Local Similarity 92.7%; Pred. No. 1e-71;  
Matches 228; Conservative 3; Mismatches 15; Indels 0; Gaps 0;  
QY 41 VOLVESGGGLVOPGGSLRLSCAASGFTFSYWMVSWRQAPGKLEWVANIKQSGSEKYYV 100  
Db 2 VOLVOSGGGLVOPGSRSLRLSCAASGFTFSYWMVSWRQAPGKLEWVANIKQSGSEKYYV 61  
QY 101 DSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARDLLKKGSSGWFDPGRTGYV 160  
Db 62 DSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARDYDILGYHDADFINGRGIMVT 121  
QY 161 VSSGGGSGGGGSGGGSSSELTQDPAVSVALLGQTVRITCGDLSRYASWYQQRPGAP 220  
Db 122 VSSGGGSGGGGSGGGSSSELTQDPAVSVALLGQTVRITCGDLSRYASWYQQRPGAP 181  
QY 221 VLVITYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVGGGT 280  
Db 182 VLVVYAKNKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVGGGT 241  
QY 281 KLTVLG 286  
Db 242 KLTVLG 247

RESULT 15  
ABG92024 standard; Protein: 263 AA.  
XX  
XX AC ABG92024;  
XX  
XX DT 04-DEC-2002 (first entry)

XX Antibody protein #4.  
DE  
XX  
KW Antibody; epitope; cancer; tumour; cell rolling; inflammation;  
KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
KW myocardial infarction; retinopathic disease; abnormal platelet function;  
KW sulphated tyrosine-dependent protein-protein interaction.  
XX  
OS Unidentified.  
PN WO200253700-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 31-DEC-2001; 2001WO-US49442.  
XX  
PR 29-DEC-2000; 2000US-258948P.  
PR 29-DEC-2000; 2000US-0751181.  
XX  
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
XX  
PI Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
PI Sznathon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
XX  
DR WPI; 2002-67476/72.  
XX  
XX Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer -  
XX  
PS Disclosure; Fig 50; 310pp; English.  
XX  
XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,  
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
CC increasing mortality of tumour or leukaemia cells, for increasing the  
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
CC or anti-leukaemia agents, or for decreasing the number of tumour or  
CC leukaemia cells in a patient, or in the manufacture of a medicament for  
CC the above mentioned purposes. The epitopes are useful for diagnosing and  
CC treating diseases such as cancer, leukaemia, autoimmune diseases,  
CC inflammatory diseases, cardiovascular diseases such as myocardial  
CC infarction, retinopathic diseases and other diseases mediated by abnormal  
CC platelet function and diseases caused by sulphated tyrosine-dependent  
CC protein-protein interactions. This sequence represents an antibody  
CC  
XX  
SQ Sequence 263 AA;  
Query Match 72.4%; Score 118; DB 23; Length 263;  
Best Local Similarity 86.4%; Pred. No. 2e-71;  
Matches 235; Conservative 5; Mismatches 16; Indels 16; Gaps 2;

QY 221 VLVIYGNKNNRPSGLPDRFGSSSGNTASLTITGAQAEDEADYCNRSDDSGNHVFGGT 280  
DB 175 VLVIYGNKNNRPSGLPDRFGSSSGNTASLTITGAQAEDEADYCNRSDDSGNHVFGGT 234  
QY 281 KLTVLGAHAHHHHHGAAGKLISEEDLNGAA 312  
DB 235 KLTVLGA-----AAEQKLISEEDLNGAA 257

Search completed: September 22, 2003, 15:18:44  
Job time : 53.2793 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 18.4318 Seconds  
(Without alignments)  
716.207 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642

Sequence: 1 MTMTTSPFGAFLEIFNVK.....HHHGAEOKLISEEDINGAA 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1642	100.0	312	US-09-079-029-10	Sequence 10, Appl
2	1460.5	88.9	309	US-09-079-029-9	Sequence 9, Appl
3	1231	75.0	310	US-09-079-029-11	Sequence 11, Appl
4	1176.5	71.7	280	US-09-260-527-1	Sequence 1, Appl
5	1037.5	63.2	278	US-09-260-527-3	Sequence 3, Appl
6	937	57.1	249	US-10-039-785-53	Sequence 53, Appl
7	850.5	51.8	284	US-09-184-658-40	Sequence 40, Appl
8	835	50.9	289	US-09-184-658-63	Sequence 63, Appl
9	827.5	50.4	284	US-08-564-164A-2	Sequence 2, Appl
10	819.5	49.9	334	US-09-646-028-53	Sequence 53, Appl
11	819.5	49.9	339	US-09-646-028-55	Sequence 55, Appl
12	815.5	49.7	348	US-09-646-028-51	Sequence 51, Appl
13	802	48.8	245	US-08-918-148-78	Sequence 78, Appl
14	798	48.6	282	US-08-860-174A-10	Sequence 10, Appl
15	795.5	48.4	301	US-08-661-052-14	Sequence 14, Appl
16	795.5	48.4	301	US-09-188-082-14	Sequence 14, Appl
17	795.5	48.4	301	US-09-364-088-14	Sequence 14, Appl
18	795.5	48.4	301	US-09-102-716-14	Sequence 14, Appl
19	795	48.4	245	US-08-918-148-75	Sequence 75, Appl
20	792	48.2	225	US-09-553-498-8	Sequence 8, Appl
21	792	48.1	255	US-09-618-869-8	Sequence 8, Appl
22	790.5	48.1	297	US-09-486-814A-2	Sequence 2, Appl
23	789	48.1	245	US-08-918-148-76	Sequence 16, Appl
24	778	47.4	359	US-09-646-028-16	Sequence 13, Appl
25	774	47.1	361	US-09-646-028-13	Sequence 77, Appl
26	760.5	46.3	244	US-08-918-148-77	Sequence 178, Appl
27	746	45.4	281	US-09-025-769B-178	

28	741.5	45.2	553	2	US-08-661-052-16	Sequence 16, Appl
29	741.5	45.2	553	3	US-09-188-082-16	Sequence 16, Appl
30	741.5	45.2	553	4	US-09-364-088-16	Sequence 16, Appl
31	741.5	45.2	553	4	US-09-102-716-16	Sequence 16, Appl
32	740.5	45.1	268	4	US-09-554-765-2	Sequence 2, Appl
33	739.5	45.0	277	2	US-08-256-790-2	Sequence 2, Appl
34	736	44.8	249	4	US-08-918-148-74	Sequence 74, Appl
35	733	44.6	258	4	US-08-665-202-5	Sequence 5, Appl
36	733	44.6	258	4	US-09-315-574-5	Sequence 5, Appl
37	725.5	44.2	244	4	US-08-918-148-79	Sequence 79, Appl
38	724	44.1	245	4	US-10-039-785-42	Sequence 42, Appl
39	724	44.1	247	3	US-09-227-693-34	Sequence 34, Appl
40	724	44.1	248	1	US-08-331-398A-34	Sequence 34, Appl
41	724	44.1	248	2	US-08-331-397B-34	Sequence 34, Appl
42	724	44.1	248	2	US-08-759-804A-34	Sequence 34, Appl
43	721.5	43.9	243	1	US-07-958-140-2	Sequence 2, Appl
44	721.5	43.9	243	5	PCT-US93-09166-2	Sequence 2, Appl
45	721	43.9	240	1	US-08-488-113B-148	Sequence 148, Appl

## ALIGNMENTS

RESULT 1  
US-09-079-029-10  
; Sequence 10, Application US/09079029  
; Patent No. 6342369  
GENERAL INFORMATION:  
; APPLICANT: Adams, Camilla W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntarapai, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079, 029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1010R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-079-029-10

Query Match 100.0%; Score 1642; DB 4; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTTSPFGAFLEIFNVKLLFAIPLVYFYAOPAMAGVOLVESGGGLVOPGGSLRLS 60  
Db 1 MTMTTSPFGAFLEIFNVKLLFAIPLVYFYAOPAMAGVOLVESGGGLVOPGGSLRLS 60  
QY 61 CAASGFTFSSYMSWVRQADPGKGLEWVANIKDGSSEKRYVDSVKGRTTISRDNKNSLYL 120

Db 61 CAASGTFSSYMSWVRQAPGKLEWVANIKODGSEKYYVDSVKGFTTISRDNKNSLYL 120  
QY 121 QMNSLRABEDTAVYYCARDLKVKSSSGMFDPWGRGRTVTVSSGGGSGGGSGGSSSE 180  
Db 121 QMNSLRABEDTAVYYCARDLKVKSSSGMFDPWGRGRTVTVSSGGGSGGGSGGSSSE 180  
QY 181 LTQDPAVSVALGQVVRITCGDLSRSYASWYQOKPGAPLVLYIGKNNRPSGIPDRFSG 240  
Db 181 LTQDPAVSVALGQVVRITCGDLSRSYASWYQOKPGAPLVLYIGKNNRPSGIPDRFSG 240  
QY 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAE 300  
Db 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAE 300  
QY 301 KLISEEDLNGAA 312  
Db 301 KLISEEDLNGAA 312

## RESULT 2

US-09-079-029-9  
; Sequence 9, Application US/09079029  
; Patent No. 6342369  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilla W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntharapal, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079.029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1101R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 309 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-079-029-9

Query Match 88.9%; Score 1460.5; DB 4; Length 309;  
Best Local Similarity 90.1%; Pred. No. 1.4e-11;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAGVOLVSSGGGLVOPGGSRLRS 60  
Db 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAGVOLVSSGGGLVOPGGSRLRS 60  
QY 61 CAASGTFSSYMSWVRQAPGKLEWVANIKODGSEKYYVDSVKGFTTISRDNKNSLYL 120  
Db 61 CAASGTFSSYMSWVRQAPGKLEWVANIKODGSEKYYVDSVKGFTTISRDNKNSLYL 120

QY 121 QMNSLRABEDTAVYYCARDLKVKSSSGMFDPWGRGRTVTVSSGGGSGGGSGGSS 179  
Db 121 QMNSLRABEDTAVYYCA---KITGAGRCWYFDLMGKGTTVTVSSGGGSGGGSGGSS 176  
QY 180 ELTOPAVSVALGQVVRITCGDLSRSYASWYQOKPGAPLVLYIGKNNRPSGIPDRFS 239  
Db 177 ELTOPAVSVALGQVVRITCGDLSRSYASWYQOKPGAPLVLYIGKNNRPSGIPDRFS 236  
QY 240 GSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAE 299  
Db 237 GSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTKLTVLGAANHNNHNGAAE 296  
QY 300 KLISEEDLNGAA 312  
Db 297 KLISEEDLNGAA 309

## RESULT 3

US-09-079-029-11  
; Sequence 11, Application US/09079029  
; Patent No. 6342369  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilla W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntharapal, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079.029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1101R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 310 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-079-029-11

Query Match 75.0%; Score 1231; DB 4; Length 310;  
Best Local Similarity 77.7%; Pred. No. 7.3e-93;  
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAGVOLVSSGGGLVOPGGSRLRS 60  
Db 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAGVOLVSSGGGLVOPGGSRLRS 60  
QY 61 CAASGTFSSYMSWVRQAPGKLEWVANIKODGSEKYYVDSVKGFTTISRDNKNSLYL 120  
Db 61 CAASGTFSSYMSWVRQAPGKLEWVANIKODGSEKYYVDSVKGFTTISRDNKNSLYL 120  
QY 121 QMNSLRABEDTAVYYCARDLKVKSSSGMFDPWGRGRTVTVSSGGGSGGGSGGSS 178  
Db 121 QMNSLRABEDTAVYYCARD-----KGIYYMDVWGKGTIVTVSSGGGSGGGSGGSS 172

```
QY 179 -SELTPDPAVSVALGOTVITCOGDSLR---SYVASWYOQKPGQAPVLYIGKNNRPSGI 234
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 OSVLQPPSVSCAPQQRWYITISCTGSSNSNAGHDVHWYQOLGTAPKLLITYDDSNRPSGV 232
QY 235 PDFFSGSSSGNTASLTITGAQAEADADYVCNSRDSGNHVEGGTKLTVLGAANHNNH 294
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 PDFFSGSRGTSASLITGLAQAEDEADYVCQSYDSLRSVFGGKTVLGAANHNNH 292
QY 295 HGAEOKLISEEDLNGAA 312
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 HGAEOKLISEEDLNGAA 310
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 4

```
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J. P.
; APPLICANT: Mikkelsen, J. D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0019.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PR1
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scfv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1
```

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Query Match 71.7%; Score 1176.5; DB 3; Length 280;
Best Local Similarity 83.3%; Pred. No. 1.8e-88;
Matches 235; Conservative 7; Mismatches 21; Indels 19; Gaps 3;
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```
QY 33 AAQPMAGYQVLESGLVQPGGSLRLSCAASGFTFSWMSWVROAPKGLEWYANIKQ 92
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 AAQPMAGYQVLESGLVQPGGSLRLSCAASGFTFSWMSWVROAPKGLEWYANIKS 75
QY 93 --DGSEKYYVDSYKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDLKYGSSSGWF 150
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 KTDGTTDYAAPVKGKRTISRDSKNTLYLQMNLSKTEDTAVYYCARKKRKAL----- 128
QY 151 DPMGCTVTVSSSGSGSGSGSGSSSELTQDPAVSVALGQTVRITCOGSLSYAS 210
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 -RMGCGTLVTVSRGSGSGSGSGSSSELTQDPAVSVALGQTVRITCOGSLRSYAS 187
QY 211 WYQQRPGQAPVLYIGKNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYVCNSRDS 270
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 WYQQRPGQAPVLYIGKNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYVCNSRDS 247
QY 271 GNHVVFGGKTLTVLGAANHNNHGAEOKLISEEDLNGAA 312
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 GNHVVFGGKTLTVLGA-----AAEOKLISEEDLNGAA 280
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 5

```
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J. P.
; APPLICANT: Mikkelsen, J. D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
```

```
; FILE REFERENCE: DY0019.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PR1
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3
```

```
Query Match 63.2%; Score 1037.5; DB 3; Length 278;
Best Local Similarity 74.0%; Pred. No. 3.9e-77;
Matches 211; Conservative 15; Mismatches 32; Indels 27; Gaps 5;
```

```
QY 33 AAQPMAGYQVLESGLVQPGGSLRLSCAASGFTF-SSYMSWVROAPKGLEWYANIK 91
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 AAQPMAGYQVLESGLVQPGGSLRLSCAASGFTFSSYMSWVROAPKGLEWYIGYIT 75
QY 92 DQSEKYYVDSYKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDLKYGSSSGWFD 151
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 YSGS--TYNPSLSKRYTMSVDTSKNOFSLKSSVTAVDYAVYCAR-----FH 122
QY 152 P---WGRCTVTVSSSGSGSGSGSGSSSELTQDPAVSVALGQTVRITCOGSLRSY 207
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 PRYDPMGCGTLTVTVSRGSGSGSGSGSSSELTQDPAVSVALGQTVRITCOGSLRSY 182
QY 208 YASWYOQKPGQAPVLYIGKNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYCNR 267
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 YASWYOQKPGQAPVLYIGKNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYCNR 242
QY 268 DSSGNHVVFGGKTLTVLGAANHNNHGAEOKLISEEDLNGAA 312
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 DSSGNHVVFGGKTLTVLGA-----AAEOKLISEEDLNGAA 278
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 6

```
US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
```

LENGTH: 249  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: T1006f07 scfv  
US-10-039-785-53

Query Match 57.1%; Score 937; DB 4; Length 249;  
Best Local Similarity 74.7%; Pred. No. 5.3e-69;  
Matches 186; Conservative 20; Mismatches 39; Indels 4; Gaps 3;

QY 41 VGLVESGGGLVPGGSLRLSCAASGFTSSYMWKRAQPGKLELVANIKQDGSRTYV 100  
DB 2 VQLVESGGGLVPGGSLRLSCAASGFTSSYAWSWRAQPGKLELVANISGSGSTYYA 61  
QY 101 DSVKGFRTISRDNKNSLYLQNMNSLRADPTAVYYCARD-LLKVGSSSGMFDPMWGRGTYY 159  
DB 62 DSVKGFRTISRDNKNSLYLQNMNSLRADPTAVYYCARDPFGQWGHYSGMDYWGQGTWY 121  
QY 160 TVSSGGGSGGSGGSGGSGSSE--LTQDPVAVSVALGQTVRTICGDSLRSYASWYQQRG 217  
DB 122 TVSSGGGSGGSGGSGGSGSAQSVLTQPPSVSVSPGQAARITCGDKLGDKYASWYQQRG 181  
QY 218 QAPVLYTYGKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYVCNSRDSSGNHYVFG 277  
DB 182 QSPVLYTYGKNNRPSGIPDRFGSSSGNTATLKTGTQAMDEADYCLAMDSADW-VFG 240  
QY 278 GGTGLTVLG 286  
DB 241 GGTGLTVLG 249

RESULT 7  
US-09-184-658-40  
Sequence 40, Application US/09184658  
Patent No. 6030792  
GENERAL INFORMATION:  
APPLICANT: Otterness, Ivan G.  
APPLICANT: Mezes, Peter S.  
APPLICANT: Downs, James T.  
APPLICANT: Johnson, Kimberly S.  
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in  
FILE REFERENCE: PC9946-A  
CURRENT APPLICATION NUMBER: US/09/184,658  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: 60/065,423  
EARLIER FILING DATE: 1997-11-13  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 40  
LENGTH: 284  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 9A4 scfv VH -  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(22)  
OTHER INFORMATION: PCANTAB6 signal peptide: Val at position 1 is most  
OTHER INFORMATION: likely the initiator Met.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (23)..(137)  
OTHER INFORMATION: 9A4 VH domain.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (138)..(152)  
OTHER INFORMATION: 15 amino acid linker.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (153)..(258)

OTHER INFORMATION: 9A4 VL domain.  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (262)..(267)  
OTHER INFORMATION: His tag.  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (271)..(280)  
OTHER INFORMATION: myc tag.  
US-09-184-658-40

Query Match 51.8%; Score 850.5; DB 3; Length 284;  
Best Local Similarity 57.9%; Pred. No. 7.1e-62;  
Matches 172; Conservative 39; Mismatches 71; Indels 15; Gaps 6;

QY 18 VKKLEAIPLVYFYFAQAPAMGVOLVESGGGLVPGGSLRLSCAASGFTSSYMWKRW 77  
DB 1 MKKLEAIPLVYFYFAQAPAMQIQLVQSGPELKKFGETVKISCKASGTTFTDYSIHVK 60  
QY 78 QAPKGLLEVANIKQDGSSEKYYVSVKGRFTISRDNKNSLYLQNMNSLRADPTAVYYCAR 137  
DB 61 QAPKGLKMWGINTETGPEPTVADDFKGFAPFSLTASATVYLQINLNKEDPTAVYYCAR 120  
QY 138 DLKVGSSSGMFDPMWGRGTYYVSSGGGSGGSGGSGSS-ELTQDPA-VSVALGQTV 195  
DB 121 -----GSLDLYWGQGTTLTVSSGGGSGGSGGSGSQITVLQSPFMSASPGERY 171  
QY 196 RITCGDSLRSYASWYQQRGQAPVLYTYGKNNRPSGIPDRFGSSSGNTASLTITGAQ 255  
DB 172 TMTCSASSSVS-YMTYQQRKPGSPRLLIHANSNLASGVYVRSGGSGSTSLTISRME 230  
QY 256 AEDADYVCNSRDSGNHNVFGGRTKLVYGAANHHHHHGAEOKLISEEDLNGAA 312  
DB 231 AEDATYYCQOWRSYTR--TFGGGTGLEIIT-AAAHHHHHGAEOKLISEEDLNGAA 284

RESULT 8  
US-09-184-658-63  
Sequence 63, Application US/09184658  
Patent No. 6030792  
GENERAL INFORMATION:  
APPLICANT: Otterness, Ivan G.  
APPLICANT: Mezes, Peter S.  
APPLICANT: Downs, James T.  
APPLICANT: Johnson, Kimberly S.  
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in  
FILE REFERENCE: PC9946-A  
CURRENT APPLICATION NUMBER: US/09/184,658  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: 60/065,423  
EARLIER FILING DATE: 1997-11-13  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 63  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(22)  
OTHER INFORMATION: PCANTAB6 signal peptide: Val at position 1 is most  
OTHER INFORMATION: likely initiator Met.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (23)..(138)  
OTHER INFORMATION: 5109 VH domain.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (139)..(154)



Query Match	49.9%	Score 819.5	DB 4	Length 334
Best Local Similarity	61.8%	Pred. No. 2.9e-59		
Matches 168	Conservative 23	Mismatches 62	Indels 19	Gaps 6
QY	33	AAQPMACVOLVESGGGGLVDPGSGIRLSCAASGFTFSSTYKMSWVAQAPGKLEVPANIKQ	92	

```
DB 73 AQAAPKSLVQLLESGGGLVQSGSLRLSCVASGLTFSSSAITWVROAPKGLWVSGISCF 132
QY 93 DGESEYVYDVKGRFTISRDNAKNSLYLQMSLRADETAVYYCARDLKVKGSSSGWF-- 150
DB 133 SCDTITVYADSVKGRFSASRDNSKNTVYLMNNLRPNDTAVYFCA-----NNQTGNFCL 185
QY 151 DPMWGCTVTVYSS--GGGSGGGSGGGGSG--SELTODPAVVAALGQVYRITCGDSLRL- 205
DB 186 DNMGGCTVTVYSSRGGGSGGGSGGSGSVLTQPPSVSAAPQQRVTISCTGSRNMI 245
QY 206 --SYTASWYQOKPGQAPVLYIGKNNRPSGIPDRFSSSGSNWASLTITGAQAEDEADY 263
DB 246 GAGYDVNMWYQKPEPTAPKVLITSNNNRPSGVPDRSGSGKSISASLATITGLQLEDEGTY 305
QY 264 CNSRDSGNNHVVFGGCTKLVLGAAAHNNHH 295
DB 306 CQCNDSDLSLGMVFGGCTKLVTL--RHNNHHH 334
```

## RESULT 11

```
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
```

## GENERAL INFORMATION:

```
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55
```

Query Match 49.9%; Score 819.5; DB 4; Length 339;

Best Local Similarity 61.8%; Pred. No. 3e-59; Matches 168; Conservative 23; Mismatches 62; Indels 19; Gaps 6;

```
QY 33 AAQPMAGVQLVESGGGLVQPGSLRLSCAASGFTFSYMWMSVROAPKGLWVANNIKQ 92
DB 78 AQAAPKSLVQLLESGGGLVQSGSLRLSCVASGLTFSSSAITWVROAPKGLWVSGISF 137
QY 93 DGESEYVYDVKGRFTISRDNAKNSLYLQMSLRADETAVYYCARDLKVKGSSSGWF-- 150
DB 138 SCDTITVYADSVKGRFSASRDNSKNTVYLMNNLRPNDTAVYFCA-----NNQTGNFCL 190
QY 151 DPMWGCTVTVYSS--GGGSGGGSGGGGSG--SELTODPAVVAALGQVYRITCGDSLRL- 205
DB 191 DNMGGCTVTVYSSRGGGSGGGSGGSGSVLTQPPSVSAAPQQRVTISCTGSRNMI 250
QY 206 --SYTASWYQOKPGQAPVLYIGKNNRPSGIPDRFSSSGSNWASLTITGAQAEDEADY 263
DB 246 GAGYDVNMWYQKPEPTAPKVLITSNNNRPSGVPDRSGSGKSISASLATITGLQLEDEGTY 310
QY 264 CNSRDSGNNHVVFGGCTKLVLGAAAHNNHH 295
DB 311 CQCNDSDLSLGMVFGGCTKLVTL--RHNNHHH 339
```

## RESULT 12

```
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
```

## GENERAL INFORMATION:

```
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51
```

Query Match 49.7%; Score 815.5; DB 4; Length 348;

Best Local Similarity 62.9%; Pred. No. 6.5e-59; Matches 166; Conservative 23; Mismatches 56; Indels 19; Gaps 6;

```
QY 41 VOLVESGGGLVQPGSLRLSCAASGFTFSYMWMSVROAPKGLWVANNIKODGSEKTYV 100
DB 95 VOLVESGGGLVQSGSLRLSCVASGLTFSSSAITWVROAPKGLWVSGISFSDTYYA 154
QY 101 DSVKGRFTISRDNAKNSLYLQMSLRADETAVYYCARDLKVKGSSSGWF--DPMGRGTT 158
DB 155 DSVKGRFSASRDNSKNTVYLMNNLRPNDTAVYFCA-----NNQTGNFCLDNMGGCTL 207
QY 159 VTVSS--GGGSGGGSGGGGSG--SELTODPAVVAALGQVYRITCGDSLRL--SYTASW 211
DB 208 VTVSSGSGGGSGGGSGGSGSVLTQPPSVSAAPQQRVTISCTGSRNIGAGYDVNM 267
QY 212 YQOKPGQAPVLYIGKNNRPSGIPDRFSSSGSNWASLTITGAQAEDEADYCNRRDSSG 271
DB 268 YQKPEPTAPKVLITSNNNRPSGVPDRSGSGKSISASLATITGLQLEDEGTYCQCNDSL 327
QY 272 NHVFGGCTKLVTLGAAAHNNHHH 295
DB 328 SGVLFGGGCTKLVTL--RHNNHHH 348
```

## RESULT 13

```
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
```

## GENERAL INFORMATION:

```
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendley, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
```

```
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78
```

Query Match 48.8%; Score 802; DB 4; Length 245;

Best Local Similarity 64.8%; Pred. No. 5.3e-58; Matches 164; Conservative 27; Mismatches 52; Indels 10; Gaps 5;



```
Db      137  VSSGGGGGGGGGGGGSDIQLTQSPSSLASVGDRTTICKSSQSQSVLYSSNQKXLYAWY 196
QY      213  QOKPGQAPVLYYGNKNNRPSGIPDRFSGSSSGNTASLTTTGAQAEDEADYCNRRDSSGN 272
        ||||:| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      197  QOKPGKAPKRLIYMASTRESGVPSRFSGGSGCTDFTFTISSLPEDIAITYCHQYLISSW- 255
QY      273  HYVEGGGTKLYLGAANH--HHHHGAABOKLISEEDLNGAA 312
        || || | | : : : : | | | | | | | | | | | | | | | | | |
Db      256  --TFGQGTKEIKSSCGGGSDIAAAEQKLISEEDLNGAA 295
```

Search completed: September 22, 2003, 15:16:01  
Job time : 19.4318 secs

Tue Sep 23 09:08:14 2003

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:16:07 : Search time 34.5177 Seconds  
(without alignments)  
1345.823 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642  
Sequence: 1 MTMTSPGAFLEIFNVKK.....HHHGAQEOKIISEDNLGAA 312Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1:  Published_Applications_AA:*
2:  /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
3:  /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep:*
4:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5:  /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1642	100.0	312	12	US-10-288-917-10
2	1642	100.0	312	14	US-10-052-798-10
3	1460.5	88.9	309	12	US-10-288-917-9
4	1460.5	88.9	309	14	US-10-052-798-9
5	1231	75.0	310	12	US-10-288-917-11
6	1231	75.0	310	14	US-10-052-798-11
7	1192	72.6	247	11	US-09-880-748-1470
8	1162	70.8	251	11	US-09-880-748-1594
9	1149	70.0	249	11	US-09-880-748-1109
10	1142	69.5	251	11	US-09-880-748-952
11	1139.5	69.3	248	11	US-09-880-748-1189
12	1138.5	69.3	248	11	US-09-880-748-916
13	1134.5	69.1	248	11	US-09-880-748-914
14	1134.5	69.1	248	11	US-09-880-748-914
15	1134	69.1	237	11	US-09-880-748-2112

16	1133.5	69.0	248	11	US-09-880-748-835
17	1133	69.0	237	11	US-09-880-748-2039
18	1133	69.0	247	11	US-09-880-748-924
19	1132.5	69.0	248	11	US-09-880-748-1323
20	1132.5	69.0	290	12	US-09-969-748C-2
21	1132.5	69.0	290	12	US-09-949-039-2
22	1127	68.6	247	11	US-09-880-748-1764
23	1125.5	68.5	240	11	US-09-880-748-1912
24	1125.5	68.5	296	12	US-09-880-748C-12
25	1125.5	68.5	296	12	US-09-949-039-75
26	1125	68.5	237	11	US-09-880-748-2006
27	1125	68.5	249	11	US-09-880-748-1724
28	1124.5	68.5	252	11	US-09-880-748-1731
29	1124	68.5	240	11	US-09-880-748-2056
30	1123.5	68.4	243	11	US-09-880-748-2013
31	1123.5	68.4	248	11	US-09-880-748-913
32	1122	68.3	239	11	US-09-880-748-2035
33	1122	68.3	249	11	US-09-880-748-2035
34	1119	68.1	239	11	US-09-880-748-1725
35	1119	68.1	247	11	US-09-880-748-1703
36	1118	68.1	243	11	US-09-880-748-1929
37	1117.5	68.1	238	11	US-09-880-748-1931
38	1117.5	68.1	248	11	US-09-880-748-920
39	1117	68.0	239	11	US-09-880-748-2022
40	1117	68.0	239	11	US-09-880-748-2023
41	1116	68.0	249	11	US-09-880-748-1817
42	1115	67.9	249	11	US-09-880-748-912
43	1115	67.9	249	11	US-09-880-748-963
44	1114	67.8	237	11	US-09-880-748-2036
45	1112	67.7	241	11	US-09-880-748-1911

## ALIGNMENTS

RESULT 1  
US-10-288-917-10  
Sequence 10, Application US/10288917  
Publication No. US20030148455A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharepal, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy diskCOMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/288,917  
FILING DATE: 06-NO. US20030148455A1-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/052798

FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029

FILING DATE: 14-MAY-1998

APPLICATION NUMBER: 60/074119

FILING DATE: 09-FEB-1998

APPLICATION NUMBER: 60/046615

FILING DATE: 15-MAY-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.

Sequence 835, App  
Sequence 2039, App  
Sequence 924, App  
Sequence 1233, App  
Sequence 2, Appl1  
Sequence 1764, App  
Sequence 1912, App  
Sequence 75, Appl  
Sequence 2006, App  
Sequence 1724, App  
Sequence 1731, App  
Sequence 2056, App  
Sequence 2013, App  
Sequence 913, App  
Sequence 2035, App  
Sequence 1725, App  
Sequence 2018, App  
Sequence 1703, App  
Sequence 1929, App  
Sequence 1931, App  
Sequence 920, App  
Sequence 2022, App  
Sequence 2023, App  
Sequence 1817, App  
Sequence 912, App  
Sequence 963, App  
Sequence 2036, App  
Sequence 1911, App

REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-288-917-10

Query Match 100.0%; Score 1642; DB 12; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.8e-109;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTITPSFGAFLEIFNVKKLLFAIPLVVFYAAOPAMAGVOLVESGGGLVOPGSLRLS 60  
DB 1 MMTITPSFGAFLEIFNVKKLLFAIPLVVFYAAOPAMAGVOLVESGGGLVOPGSLRLS 60  
QY 61 CAASGFTFSYMSWVRQAPGKGLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120  
DB 61 CAASGFTFSYMSWVRQAPGKGLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120  
QY 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGRTTVVSSGGGSGGGSGSSSE 180  
DB 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGRTTVVSSGGGSGGGSGSSSE 180  
QY 181 LTQDPVAVSALGTVTRTCGDSLRSYASWYQOKRQAPVLYTYGKNNRPSGIPDRFSG 240  
DB 181 LTQDPVAVSALGTVTRTCGDSLRSYASWYQOKRQAPVLYTYGKNNRPSGIPDRFSG 240  
QY 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAAGAAHHHHGAAG 300  
DB 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAAGAAHHHHGAAG 300  
QY 301 KLISEEDLNGAA 312  
DB 301 KLISEEDLNGAA 312

RESULT 2  
US-10-052-798-10  
Sequence 10, Application US/10052798  
Publication No. US20020150985A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/052,798  
FILING DATE: 02-No. US20020150985A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-052-798-10

Query Match 100.0%; Score 1642; DB 14; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.8e-109;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTITPSFGAFLEIFNVKKLLFAIPLVVFYAAOPAMAGVOLVESGGGLVOPGSLRLS 60  
DB 1 MMTITPSFGAFLEIFNVKKLLFAIPLVVFYAAOPAMAGVOLVESGGGLVOPGSLRLS 60  
QY 61 CAASGFTFSYMSWVRQAPGKGLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120  
DB 61 CAASGFTFSYMSWVRQAPGKGLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120  
QY 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGRTTVVSSGGGSGGGSGSSSE 180  
DB 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGRTTVVSSGGGSGGGSGSSSE 180  
QY 181 LTQDPVAVSALGTVTRTCGDSLRSYASWYQOKRQAPVLYTYGKNNRPSGIPDRFSG 240  
DB 181 LTQDPVAVSALGTVTRTCGDSLRSYASWYQOKRQAPVLYTYGKNNRPSGIPDRFSG 240  
QY 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAAGAAHHHHGAAG 300  
DB 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAAGAAHHHHGAAG 300  
QY 301 KLISEEDLNGAA 312  
DB 301 KLISEEDLNGAA 312

RESULT 3  
US-10-288-917-9  
Sequence 9, Application US/10288917  
Publication No. US20030148455A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/288,917  
FILING DATE: 06-No. US20030148455A1-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 10/052798  
FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029  
FILING DATE: 14-MAY-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-FEB-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-288-917-9

Query Match 88.9%; Score 1460.5; DB 12; Length 309;  
Best Local Similarity 90.1%; Pred. No. 2.2e-96;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;  
QY 1 MTMTPTSGAFLEIFENYKLLFALPLVPPYAPAPAGVQLVSGGGLVOPGSLRLS 60  
DB 1 MTMTPTSGAFLEIFENYKLLFALPLVPPYAPAPAEVQLVSGGGLVOPGSLRLS 60  
QY 61 CAASGFTTSSYWMNVROAPGKGLVEMVANI KODGSEKYYVSVKGRFTISRDNKNSLYL 120  
DB 61 CAASGFTTDDYGMVSVROAPGKGLVEMVANI KODGSEKYYVSVKGRFTISRDNKNSLYL 120  
QY 121 QMNSLRADPTAVYYCAKDLKLVKSSSGW-FDPMGRGTTVTVSSGGGGSGGGSGGSS 179  
DB 121 QMNSLRADPTAVYYCAKDLKLVKSSSGW-FDPMGRGTTVTVSSGGGGSGGGSGGSS 176  
QY 180 ELTODPAVVALGOTVRITCGDLSRYSYASMYOQKPGQAPVLVYGNKNNPSGIPDFRS 239  
DB 177 ELTODPAVVALGOTVRITCGDLSRYSYASMYOQKPGQAPVLVYGNKNNPSGIPDFRS 236  
QY 240 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVYGAHHHHHNGAAE 299  
DB 237 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVYGAHHHHHNGAAE 296  
QY 300 OKLISEEDLNGAA 312  
DB 297 OKLISEEDLNGAA 309

RESULT 4  
US-10-052-798-9  
Sequence 9, Application US/10052798  
Publication No. US20020150985A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapal, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/052,798  
FILING DATE: 02-NO. US20020150985A1-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-052-798-9

Query Match 88.9%; Score 1460.5; DB 14; Length 309;  
Best Local Similarity 90.1%; Pred. No. 2.2e-96;  
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;  
QY 1 MTMTPTSGAFLEIFENYKLLFALPLVPPYAPAPAGVQLVSGGGLVOPGSLRLS 60  
DB 1 MTMTPTSGAFLEIFENYKLLFALPLVPPYAPAPAEVQLVSGGGLVOPGSLRLS 60  
QY 61 CAASGFTTSSYWMNVROAPGKGLVEMVANI KODGSEKYYVSVKGRFTISRDNKNSLYL 120  
DB 61 CAASGFTTDDYGMVSVROAPGKGLVEMVANI KODGSEKYYVSVKGRFTISRDNKNSLYL 120  
QY 121 QMNSLRADPTAVYYCAKDLKLVKSSSGW-FDPMGRGTTVTVSSGGGGSGGGSGGSS 179  
DB 121 QMNSLRADPTAVYYCAKDLKLVKSSSGW-FDPMGRGTTVTVSSGGGGSGGGSGGSS 176  
QY 180 ELTODPAVVALGOTVRITCGDLSRYSYASMYOQKPGQAPVLVYGNKNNPSGIPDFRS 239  
DB 177 ELTODPAVVALGOTVRITCGDLSRYSYASMYOQKPGQAPVLVYGNKNNPSGIPDFRS 236  
QY 240 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVYGAHHHHHNGAAE 299  
DB 237 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVYGAHHHHHNGAAE 296  
QY 300 OKLISEEDLNGAA 312  
DB 297 OKLISEEDLNGAA 309

RESULT 5  
US-10-288-917-11  
Sequence 11, Application US/10288917  
Publication No. US20030148455A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapal, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/288,917
  FILING DATE: 06-NOV. US20030148455A1-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 10/052798
  FILING DATE: 02-NOV-2001
  APPLICATION NUMBER: 09/079029
  FILING DATE: 14-MAY-1998
  APPLICATION NUMBER: 60/074119
  FILING DATE: 09-FEB-1998
  APPLICATION NUMBER: 60/046615
  FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
  REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 310 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-288-917-11
```

Query Match 75.0%; Score 1231; DB 12; Length 310;

Best Local Similarity 77.7%; Pred. No. 4.5e-80;

Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

```
OY 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAAQPMAGVOLYESGGGLVOPGSLRLS 60
DB 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAAQPMAGVOLYESGGGLVOPGSLRLS 60
OY 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
DB 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
OY 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
DB 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
OY 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
DB 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
OY 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
DB 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
OY 179 -SELTQDPAVSALGQTVRITCOGDSLR---SYASWYQKPGQAPVLVIYGNKRRPSGI 234
DB 173 OSVLQPPSVSGAPQGRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV 232
OY 235 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 294
DB 233 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 292
OY 235 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 294
DB 233 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 292
OY 295 HGAAPQKLISEEDLNGAA 312
DB 293 HGAAPQKLISEEDLNGAA 310
```

## RESULT 6

US-10-052-798-11

Sequence 11, Application US/10052798

Publication No. US20020150985A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

Chuntharapai, Anan

Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

```
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/052,798
  FILING DATE: 02-NOV. US20020150985A1-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/079,029
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
  REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 310 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-052-798-11
```

Query Match 75.0%; Score 1231; DB 14; Length 310;

Best Local Similarity 77.7%; Pred. No. 4.5e-80;

Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

```
OY 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAAQPMAGVOLYESGGGLVOPGSLRLS 60
DB 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAAQPMAGVOLYESGGGLVOPGSLRLS 60
OY 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
DB 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
OY 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
DB 61 CAASGFTSSYTWMSNVRAPGKGLVEMVANI KODGSEKYYVSVKGRFTISDNKNSLYL 120
OY 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
DB 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
OY 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
DB 121 QMNSLRADPTAVYVCARLKLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGGS 178
OY 179 -SELTQDPAVSALGQTVRITCOGDSLR---SYASWYQKPGQAPVLVIYGNKRRPSGI 234
DB 173 OSVLQPPSVSGAPQGRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV 232
OY 235 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 294
DB 233 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 292
OY 235 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 294
DB 233 PDRESGSSGNTASLTITGAQAEDBADYYCNSRDSSGNHVVFGGCTKLTVLGAANHHNH 292
OY 295 HGAAPQKLISEEDLNGAA 312
DB 293 HGAAPQKLISEEDLNGAA 310
```

## RESULT 7

US-09-880-748-1470

Sequence 1470, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

FILE REFERENCE: P523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17



```
Query Match      70.8%; Score 1162; DB 11; length 251;
Best Local Similarity 88.8%; Pred. No.2.9e-75;
Matches 222; Conservative 10; Mismatches 14; Indels 4; Gaps 1
```

OY	4	VOLVESGGGVOPGGGLRLRSCASAGFTFSSYMSWVROAPGKLEPMVINIKDSEKKYY	100
Dd	2	VOLVESGGGVVPQGRSLRLSCASAGFTFESSYMHHVROAPGKLEMAVAISTDSNKKYY	61
OY	101	DSYKGRTTISRDNAKNSLYLQMNLSLAEDTAAYYCARG--DLKVKSGSSSGWFDPWGRC	156
Dd	62	DSYKGRTTISRDNKSNTLYLQNMSLAEDTAAYYCARSYDIL--TTYRKGAEDIMWOG	119
OY	157	TMYTVSSGGGSGGGGSGSSSELTOPPAVSALGQYVRITTCQDSLRSITYASHYOOKP	210
Dd	120	TMYTVSSGGGSGGGGSGGGSSSELTOPPAVSVALGQYVRITTCQDSLRSITYASHYOOKP	178
OY	217	GQAPVLVIYTKNNRPSPGIPDRFGSSSSGTASLTJTGQAEDPADYCYNSNRDSSGNHYE	278
Dd	180	GQAPVLVIYTKNNRPSGPIDRFSGSSSGTASLTJTGQAEDPADYCYNSNRDSSGNHYE	235
OY	277	GGGTKLTVLG	286
Dd	240	GGGTKLTVLG	249
RESULT	10		

```
US-09-880-748-952
; Sequence 952, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 952
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-952
```

```
Query Match      70.0%; Score 1149; DB 11; Length 251;
Best Local Similarity 88.8%; Pred. No. 2.4e-74;
Matches 222; Conservative 8; Mismatches 16; Indels 4; Gaps 1;
```

```
QY 41 VOLVESGGGLVQPGGSLRLSCAASGFTFSSTWMSWVRQAPGKGLEWYANIKDGSSEKYYV 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLVQSSGGGVQPGGSLRLSCAASGFTFSSTWMSWVRQAPGKGLEWYAFIRYDGSNNYYA 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 101 DSVKGRFTISRDNKNSLYLQMNSLRRAEDTAVYYCARDL-----LKVSGSSSGMFPDPMGRG 156
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 DSVKGRFTISRDNKNSLYLQMNSLRRAEDTAVYYCARDLPYYDILTGYSLSLGMVWVRG 121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 157 TTVTVSSGGGGGGGGGGSSSELTQDPAVSVALGQTVRTTCGDSLRSYASWYQOKP 216
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 TLTVVSSGGGGGGGGGGSSSELTQDPAVSVALGQTVRTTCGDSLRSYASWYQOKP 181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 217 GQAPVLYIYGKNNRPSGIPDRFSSSSSGNTASLTITGAQADEADYYCNSRDSSGNHYVF 276
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 GQAPVLYIYGKNNRPSGIPDRFSSSSSGNTASLTITGAQADEADYYCNSRDSSGNHYVF 241
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 277 GGGTKLTVLG 286
      |||:|||||:
Db 242 GGGTKLTVLG 251
```

```
RESULT 11
US-09-880-748-982
; Sequence 982, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
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; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 982
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-982
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Query Match      69.5%; Score 1142; DB 11; Length 251;
Best Local Similarity 88.4%; Pred. No. 7.6e-74;
Matches 221; Conservative 8; Mismatches 17; Indels 4; Gaps 1;
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```
QY 41 VOLVESGGGLVQPGGSLRLSCAASGFTFSSTWMSWVRQAPGKGLEWYANIKDGSSEKYYV 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLVQSSGGGVQPGGSLRLSCAASGFTFSSTWMSWVRQAPGKGLEWYAFIRYDGSNNYYA 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 101 DSVKGRFTISRDNKNSLYLQMNSLRRAEDTAVYYCARDL-----LKVSGSSSGMFPDPMGRG 156
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 DSVKGRFTISRDNKNSLYLQMNSLRRAEDTAVYYCARDLPYYDILTGYSLSLGMVWVRG 121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 157 TTVTVSSGGGGGGGGGGSSSELTQDPAVSVALGQTVRTTCGDSLRSYASWYQOKP 216
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 TLTVVSSGGGGGGGGGGSSSELTQDPAVSVALGQTVRTTCGDSLRSYASWYQOKP 181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 217 GQAPVLYIYGKNNRPSGIPDRFSSSSSGNTASLTITGAQADEADYYCNSRDSSGNHYVF 276
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 GQAPVLYIYGKNNRPSGIPDRFSSSSSGNTASLTITGAQADEADYYCNSRDSSGNHYVF 241
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 277 GGGTKLTVLG 286
      |||:|||||:
Db 242 GGGTKLTVLG 251
```

```
RESULT 12
US-09-880-748-1189
; Sequence 1189, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1189
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1189

Query Match      69.4%; Score 1139.5; DB 11; Length 256;
Best Local Similarity 87.1%; Pred. No. 1.2e-73;
Matches 222; Conservative 6; Mismatches 18; Indels 9; Gaps 2;
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Query Match 69.1%; Score 1134; DB 11; Length 237;  
Best Local Similarity 89.4%; Pred. No. 2.7e-73;  
Matches 220; Conservative 4; Mismatches 12; Indels 10; Gaps 1;

QY 41 VOLVESGGGLVOPGGSLRLSCAASGFTFSYWMWVROAPGKGLEWVANIKODGSEKYYV 100  
|||:|||||  
Db 2 VOLVDSGGGLVOPGGSLRLSCAASGFTFSYWMWVROAPGKGLEWVSTISSGSTIYYA 61  
|||:|||||

QY 101 DSVKGRFTISRDNANKSLYLQMNLSLRAEDTAVYCCARDLLKYKSSSGWFDPWGRGTVT 160  
|||:|||||  
Db 62 DSVKGRFTISRDNANKSLYLQMNLSLRAEDTAVYCCARDT-----DYMGGTTRYT 111  
|||:|||||

QY 161 VSSGGGGSGGGSSGSELTPDPAYVALGQTVARITCQDPSLSYASWTQKFGQAP 220  
|||:|||||  
Db 112 VSSGGGGSGGGSSGSELTPDPAYVALGQTVARITCQDPSLSYASWTQKFGQAP 171  
|||:|||||

QY 221 VLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFGGGT 280  
|||:|||||  
Db 172 VLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFGGGT 231  
|||:|||||

QY 281 KLTVLG 286  
|||:|||||  
Db 233 KLTVLG 237  
|||:|||||

Search completed: September 22, 2003, 15:36:24  
Job time : 35.5177 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 21.1128 seconds  
(without alignments)  
1421.159 Million cell updates/sec

Title: US-10-052-798-10  
Perfect score: 1642  
Sequence: 1 MTWTFSGAFLEIFNVK.....HHHGAERKLISEEDLNGAA 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714.5	43.5	268	2 A56446	Ig heavy chain V r
2	578	35.2	249	2 S41374	Single chain Fv an
3	568	34.6	109	2 S19663	Ig lambda chain V
4	562	34.2	108	2 S47184	Ig lambda chain -
5	561	34.2	122	2 S31675	Ig heavy chain V r
6	559	34.0	147	2 I37780	Ig variable region
7	556	33.9	136	2 S31587	Ig heavy chain V r
8	552.5	33.6	117	2 S78486	Ig heavy chain V r
9	551.5	33.6	110	2 S36272	Ig lambda chain V
10	546.5	33.3	139	2 I37781	Ig variable region
11	546	33.3	127	2 S70444	Ig lambda chain pr
12	541	32.9	108	2 S38498	Ig lambda chain -
13	539	32.8	109	2 S38496	Ig lambda chain -
14	530	32.3	233	2 S25748	Ig lambda chain -
15	530	32.3	233	2 JC5322	Ig lambda chain -
16	527	32.1	108	1 L3H05H	p33 specific singl
17	522.5	31.8	123	2 S31509	Ig lambda chain V-
18	518.5	31.6	110	2 S19672	Ig heavy chain - h
19	517.5	31.5	146	2 S02083	Ig lambda chain V
20	511	31.1	114	2 S36280	Ig lambda chain V-
21	511	31.1	140	2 S70442	Ig heavy chain pre
22	510.5	31.1	140	2 S22657	Ig heavy chain pre
23	510	31.1	98	2 PL0123	Ig heavy chain V-I
24	510	31.1	117	2 S71079	Ig heavy chain V-g
25	509	31.0	110	2 PH1655	Ig heavy chain V r
26	505	30.8	122	2 E36005	Ig heavy chain V r
27	505	30.8	128	2 E36005	Ig heavy chain V r
28	504.5	30.7	119	2 D36005	Ig heavy chain V r
29	504	30.7	128	2 S26786	Ig heavy chain V r

30	503	30.6	96	2 S36060	Ig lambda chain -
31	503	30.6	115	2 S13726	Ig lambda chain V r
32	502.5	30.6	121	2 S19666	Ig heavy chain V r
33	502	30.6	233	2 S25741	Ig lambda chain -
34	497.5	30.3	121	2 G36005	Ig heavy chain V r
35	497	30.3	128	2 S48797	Ig heavy chain V r
36	496	30.2	97	2 PH0872	Ig heavy chain V r
37	496	30.2	114	2 S46390	Ig heavy chain V r
38	495.5	30.2	119	2 F36005	Ig heavy chain V r
39	495	30.1	139	2 S31674	Ig heavy chain V r
40	494.5	30.1	135	2 S31598	Ig heavy chain V r
41	494	30.1	120	2 S48798	Ig heavy chain V r
42	494	30.1	122	2 S31117	Ig heavy chain - h
43	493.5	30.1	132	2 S31603	Ig heavy chain V r
44	493	30.0	141	2 S31669	Ig heavy chain V r
45	492.5	30.0	119	2 C36005	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity dioxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 43.5%, Score 714.5; DB 2: Length 268;

Best Local Similarity 53.1%, Pred. No. 1.4e-41;

Matches 147; Conservative 38; Mismatches 81; Indels 11; Gaps 5;

Oy	38	MAGVQLVESGGGLVPGPGLRLSCAASGFTFSYWMVVRQAPGKLEWVNIKODGSEK	97
Db	1	MAQVKLOESGAEIVKPGASVRLSCTTSFENIKDTYMHVVKRPGGLEWIRIAPANGIT	60
Oy	98	YVDSVYGRFTISDNKNSLYIQMNSLRADTAIVYCCARDLKVKGSSGMPDPWGRGT	157
Db	61	KYDPKFOGKATIAADTSNTAVYQLSSLSLSEDFAVVYCASVYL-----TRYENVWGCGT	114
Oy	158	TVTVSSGGGSGGSGGSGGSS-ELTQDPV-STAAGTVITTCQGDLSRYVSWVOOK	215
Db	115	TVTVSSGGGSGGSGGSGGSDIBLTQSPALMSASLGERKYMSCRASSSV-FTYWOOK	173
Oy	216	PGQAPVLYIVYKRRPGGIPRFGSSSGNTASTLTITGAQADADYVCNSRSGNHV	275
Db	174	SDASPKLVYITSHLPGRVPRFSGSGSGSNSTLTISMEEDATYYCQGFSS--PFT	231
Oy	276	FGGQTKLVIGAAAHNNHNGAEOKLISEEDLNGAA	312
Db	232	FGSGTKLEIKRSAAHNNHNGAEOKLISEEDLNGAA	268

## RESULT 2

S41374  
single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C:Accession: S41374

R:Artsenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv anti

A:Reference number: S41374



F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 34.0%; Score 559; DB 2; Length 147;

Best Local Similarity 80.0%; Pred. No. 2.7e-31;

Matches 108; Conservative 5; Mismatches 8; Indels 14; Gaps 2;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 100

DB 15 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYA 74

QY 101 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDLKVKSSGSGW-----FDPW 153

DB 75 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDK-----GEGWGLVYXXYMDWV 127

QY 154 GRGFTVYSSGGGS 168

DB 128 GCGTIVYSSGSASA 142

#### RESULT 7

S31587

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31587

R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31587

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: EMBL:Z14189; NID:g31005; PIDD:CAA76558.1; PID:g31006

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-114/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 556; DB 2; Length 136;

Best Local Similarity 86.6%; Pred. No. 3.9e-31;

Matches 109; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 100

DB 18 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 77

QY 101 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDLKVKSSGSGWDPWGRGTYV 160

DB 78 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARGLT---GATDAFDIMGQTYV 133

QY 161 VSS 163

DB 134 VSS 136

#### RESULT 8

S78486

Ig heavy chain V region (clone FLJ3-28) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 21-Jan-2000

C:Accession: S78486; S31115

R:Raaphorst, F.M.

submitted to the EMBL Data Library, October 1991

A:Reference number: S78486

A:Accession: S78486

A:Molecule type: mRNA

A:Residues: 1-117 <RA>

A:Cross-references: EMBL:X62965

R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31115

A:Molecule type: mRNA

A:Residues: 1-4,'L','6-32','G','34-52','E','54-73','K','75-97 <RA>

A:Cross-references: EMBL:X62965

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 33.6%; Score 552.5; DB 2; Length 117;

Best Local Similarity 87.8%; Pred. No. 5.8e-31;

Matches 108; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 100

DB 2 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 61

QY 101 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDLKVKSSGSGWDPWGRGTYV 160

DB 62 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDK-----GRGSLDYWGQGLTYV 114

QY 161 VSS 163

DB 115 VSS 117

#### RESULT 9

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C:Accession: S36272

R:Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries

A:Reference number: S36236; MUID:93178448; PMID:7679990

A:Accession: S36272

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Cross-references: EMBL:Z18833; NID:g33419; PIDD:CAA79285.1; PID:g939912

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 33.6%; Score 551.5; DB 2; Length 110;

Best Local Similarity 98.2%; Pred. No. 6.4e-31;

Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 178 SSELTPQDPVAVSALGQTVRITCGGDSLSRYASWYQKPGQAPVLYIGKNNRPSGIPDR 237

DB 1 SSELTPQDPVAVSALGQTVRITCGGDSLSRYASWYQKPGQAPVLYIGKNNRPSGIPDR 60

QY 238 FSGSSSGNTASLTITGAQAEDEADYICNSRSSGN-HVFGGKTLFVLG 286

DB 61 FSGSSSGNTASLTITGAQAEDEADYICNSRSSGNLYVFGGKTLFVLG 110

#### RESULT 10

I37781

Ig variable region (VDJ) (clone T21-9) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 23-Jul-1999

C:Accession: I37781; S25475

R:Demaison, C.; Chastagner, P.; There, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A:Title: Somatic diversification in the heavy chain variable region genes expressed b

A:Reference number: A36876; MUID:94119917; PMID:8290556

A:Accession: I37781

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <RES>

A:Cross-references: EMBL:X67908; NID:g33560; PIDD:CAA48106.1; PID:g33581

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 33.3%; Score 546.5; DB 2; Length 139;  
Best Local Similarity 87.0%; Pred. No. 1.8e-30;  
Matches 107; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

QY 41 VOLVESGGILNPGGSLRLSCAASGFTSSYMSWRQAPGKLEWVANIKODGSKYYV 100  
|||||  
DB 22 VOLVESGGILNPGGSLRLSCAASGFTSSYMSWRQAPGKLEWVANIKODGSKYYV 81  
QY 101 DSVKGFRTISRDAKSLYLQMNSLRAEDTAAYYCARDLLKYVSSSGWFDPKRGCTPYE 160  
|||||  
DB 82 DSVKGFRTISRDAKSLYLQMNSLRAEDTAAYYCAR-----KRAKKAFLNMGQTMVT 136  
QY 161 VSS 163  
|||  
DB 137 VSS 139

#### RESULT 11

S70444  
Ig lambda chain precursor V region - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000  
C:Accession: S70444; S70426  
R:CluSinter, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.  
Mol. Immunol. 29, 1363-1373, 1992  
A:Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of B  
A:Reference number: S70442; MUID:93024508; PMID:1383695  
A:Accession: S70444  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-127 <CUI>  
A:Experimental source: clone E29.1  
R:Tonnelle, C.  
submitted to the EMBL Data Library, May 1990  
A:Reference number: S70426  
A:Accession: S70426  
A:Molecule type: mRNA  
A:Residues: 1-90 <TON>  
A:Cross-references: EMBL:X53070  
A:Experimental source: cell line E29.1, clone VL 29-1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:1-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>  
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 33.3%; Score 546; DB 2; Length 127;  
Best Local Similarity 97.2%; Pred. No. 1.7e-30;  
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 178 SSELTDPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYCKNNRPSGIPDR 237  
|||||  
DB 20 SSELTDPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYCKNNRPSGIPDR 79  
QY 238 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVFGGKTLVL 285  
|||||  
DB 80 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVFGGKTLVL 127

#### RESULT 12

S38498  
Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S38498  
R:Harris, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.  
submitted to the EMBL Data Library, June 1993  
A:Description: Human antibody fragments specific for human blood group antigens from a B  
A:Reference number: S38498  
A:Accession: S38498  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-108 <MAR>  
A:Cross-references: EMBL:Z23035; NID:9414043; PIDN:CAA80570.1; PID:9414044  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 541; DB 2; Length 108;  
Best Local Similarity 97.2%; Pred. No. 3.2e-30;  
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 179 SSELTDPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYCKNNRPSGIPDR 238  
|||||  
DB 1 SSELTDPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYCKNNRPSGIPDR 60  
QY 239 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVFGGKTLVLG 286  
|||||  
DB 61 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVFGGKTLVLG 108

#### RESULT 13

S38496

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S38496  
R:Harris, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.  
submitted to the EMBL Data Library, June 1993  
A:Description: Human antibody fragments specific for human blood group antigens from  
A:Reference number: S38488  
A:Accession: S38496  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109 <MAR>  
A:Cross-references: EMBL:Z23031; NID:9414039; PIDN:CAA80566.1; PID:9414040  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match 32.8%; Score 539; DB 2; Length 109;  
Best Local Similarity 93.6%; Pred. No. 4.4e-30;  
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 178 SSELTDPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYCKNNRPSGIPDR 237  
|||||  
DB 1 SSELTDPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYCKNNRPSGIPDR 60  
QY 238 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVFGGKTLVLG 286  
|||||  
DB 61 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVFGGKTLVLG 109

#### RESULT 14

S25748

Ig lambda chain - human

C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25748  
R:Combratio, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25748  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-233 <COM>  
A:Cross-references: EMBL:X57813; NID:933725; PIDN:CAA40950.1; PID:933726  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 32.3%; Score 530; DB 2; Length 233;  
Best Local Similarity 91.7%; Pred. No. 4e-29;



Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 178 SSELTPDPAVSVALGQTVRITCCGDSLRSYASWYQKPGQAPVLVIYCKNNRPSGIPDR 237

Db 20 SSELQDPAYVALGQIVRITCQGDSLRAYYASWYQHKPGQAPILVIYGENNRPSGIDR 79

238 FSGSSSGNTASTLTITGAQAEDEADYYCNSRDSSGNHVFEGGTFKLTVLG 286

Db 80 FSGSSSGNTASFAITGAQAEDADYYCNSRDSSGQVLFGGGTLTVLG 128

**RESULT 15**

JC5322

p53 specific single-chain antibody Pab421 - human

C;Species: Homo sapiens (man)  
C;Date: 15-May-1997 #sequence

C/Accession: JC5322  
C/date: 15-May-1997 #sequence\_revision 15-May-1997  
C/Accession: JC5322  
C/date: 15-May-1997 #text\_change 18-Jul-1997

R; Jannot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A; Title: Characterization of scFv-421, a single-chain antibody against the *Yersinia enterocolitica* O:3 strain 480/90.

A:Accession: JC5322  
A:Reference number: JC5322; MUID:9/168950; PMID:9016/5/

A: molecule type: mRNA

A;ResIdues: 1-233 &lt;JJA

**A; Experimental source:**

c;comment: This protein

Query Match	32.38: Score
-------------	--------------

Best Local Similarity 46.68; Pred. NO. 4e-29;

Matches 115; Conservative 36; Mismatches 74; Indels

00 45 ECCCCI IODCCSI BI CCA A CCEEECCVIA/CIA/IDOA DCCCI EPIVIA NTVODCCCEVUVUDCIUR 104

45 ESGGGLVPGGSLRLSCAASGFTSSYWMSWKQAPGKGLENVANIKQDGESEKYYVDSK 104

[illegible]

QY 105 GRTISRDNAKNSLYLQMSLR AEDTAVYYCARDLLKVKGSSSGWEDPWGRGTTVTSSG 16

Db 62 VKATMTADTSSNTAYLQLSSLTSEDTAVYYC-----NAGMDYWGQGT<sup>1</sup>TVVSSG 110

QV 165 GGGGGGGGGGGSS-ELTDPA-VSVALGOTVRITCOGD---SLRSY-YASWYOOKPGO 218

Db 111 GGGGGRASGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQOKPGQ 1700

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

171 BBPITVIVSNIESGVAPBESCSCTDEETI NIUDVEEEDAAATVVCOUTBEI MBCE-... 336

DB I/I PPRLLIYLVSNLESGVPARFSGSGGIDFTLNHPVEEDAIYYCQIRELIRSE---- 226

07  
402 A RTNOC 8/2  
: |||||  
|||

Db 227 GGTKEI 233

Search completed: September 22, 2003, 15:14:58  
Job time : 21.128 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:03 ; Search time 11.7293 Seconds

(without alignments)  
1250.910 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642

Sequence: 1 MTMTIPSGAFLLEIFNVKK.....HHGAAEQKLISEDLNCA 312

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	32.1	108	1	LV3A_HUMAN
2	468	28.5	116	1	HV3T_HUMAN
3	454	27.6	122	1	HV3G_HUMAN
4	447	27.2	114	1	HV3B_HUMAN
5	446	27.2	126	1	HV3K_HUMAN
6	437	26.6	119	1	HV38_HUMAN
7	436.5	26.6	121	1	HV3J_HUMAN
8	433	26.4	117	1	HV3C_HUMAN
9	430.5	26.2	119	1	HV3I_HUMAN
10	429	26.1	122	1	HV3H_HUMAN
11	427.5	26.0	115	1	HV3E_HUMAN
12	427	26.0	136	1	HV16_MOUSE
13	418.5	25.5	115	1	HV3D_HUMAN
14	418.5	25.5	123	1	HV18_MOUSE
15	418	25.5	119	1	HV3M_HUMAN
16	418	25.5	119	1	HV3N_HUMAN
17	417	25.4	111	1	HV35_MOUSE
18	416.5	25.4	116	1	HV05_CARAU
19	416.5	25.4	142	1	HV01_RAT
20	414.5	25.2	123	1	HV19_MOUSE
21	414	25.2	122	1	HV20_MOUSE
22	414	25.2	122	1	HV3A_HUMAN
23	413.5	25.2	123	1	HV25_MOUSE
24	413	25.2	119	1	HV37_MOUSE
25	413	25.2	122	1	HV21_MOUSE
26	412.5	25.1	120	1	HV3E_HUMAN
27	412	25.1	119	1	HV40_MOUSE
28	411.5	25.1	117	1	HV41_MOUSE
29	410.5	25.0	117	1	HV23_MOUSE
30	410	25.0	123	1	HV54_MOUSE
31	409	24.9	120	1	HV3U_HUMAN
32	406.5	24.8	113	1	HV30_MOUSE
33	406.5	24.8	115	1	HV32_MOUSE

34	406	24.7	114	1	HV01_CANFA	P01784 canis fam11
35	405.5	24.7	118	1	HV39_MOUSE	P01809 mus musculu
36	405	24.7	98	1	HV57_MOUSE	P18528 mus musculu
37	402.5	24.5	113	1	HV31_MOUSE	P01800 mus musculu
38	402.5	24.5	123	1	HV22_MOUSE	P01791 mus musculu
39	401.5	24.5	144	1	HV26_MOUSE	P01791 mus musculu
40	400.5	24.4	119	1	HV31_HUMAN	P01773 homo sapien
41	399.5	24.3	113	1	HV27_MOUSE	P01796 mus musculu
42	399.5	24.3	123	1	HV24_MOUSE	P01793 mus musculu
43	399	24.3	117	1	HV55_MOUSE	P18526 mus musculu
44	396	24.1	115	1	HV3S_HUMAN	P01780 homo sapien
45	395.5	24.1	97	1	HV56_MOUSE	P18527 mus musculu

ALIGNMENTS

RESULT 1					ALIGNMENTS				
ID	LV3A_HUMAN	STANDARD:	PRT:	108 AA.					
AC	P01714:								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	15-SEP-2003 (Rel. 02, Last annotation update)								
DE	Ig lambda chain V-II region SH.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE.								
RX	MEDLINE=70166723; PubMed=490564;								
RA	Titani K., Wikler M., Shindoda T., Putnam F.W.;								
RT	The amino acid sequence of a lambda type Bence-Jones protein. 3. The								
RT	complete amino acid sequence and the location of the disulfide								
RT	bridges.";								
RL	J. Biol. Chem. 245:2171-2176(1970).								
CC	1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.								
CC	1- SIMILARITY: Contains 1 immunoglobulin-like domain.								
DR	PIR, A01980; L3HUSH.								
DR	HSSP: F80748; ZLOT.								
DR	GO: GO:0005576; C:extracellular; NAS.								
DR	GO: GO:0003823; F:antigen binding activity; NAS.								
DR	GO: GO:0006955; P:immune response; NAS.								
DR	InterPro: IPR007110; Ig-like.								
DR	InterPro: IPR003006; Ig_MHC.								
DR	InterPro: IPR003596; Ig_V.								
DR	Pfam: PF00047; Ig_1.								
DR	SMART: SM00406; IGV; 1.								
DR	PROSITE: PS50835; IG_LIKE; 1.								
KW	Immunoglobulin V region; Bence-Jones protein.								
FT	DOMAIN 1 97								
FT	DISULFID 21 86								
FT	NON_TER 108								
FT	SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;								
Query Match									
Best Local Similarity 32.1%; Score 527; DB 1; Length 108;									
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;									
OY	179	SETLDDPAVSVALGTVRITCGDLSRSYYSWYQKPGQAPVLVIYGNRPSPGIPRF	238						
DB	1	SETLDDPAVSVALGTVRITCGDLSRGTDAWYQKPGQAPVLVIYGNRPSPGIPRF	60						
OY	239	SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVPFGGKTLTVLG	286						
DB	61	SGSSSGHTASLTITGAQAEDEADYYCNSRDSSGKHYLFGGKTLTVLG	108						
RESULT 2									
ID	HV3T_HUMAN	STANDARD:	PRT:	116 AA.					
AC	P01781:								

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=75059123; PubMed=4803843;
RX Matanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglubulin Gal.), II: the amino acid sequence of the H-chain (mu-
type), subgroup H III. Architecture of the complete IgM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR HSSP: A02064; M3HUGL.
DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-Like.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 28.5%; Score 468; DB 1; Length 116;
Best Local Similarity 74.4%; Pred. No. 2e-27;
Matches 93; Conservative 8; Mismatches 12; Indels 12; Gaps 2;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYWMVWRQAPGKLEWVANIKODGSEKYYV 100
ID HV33_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:

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RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02051; M3HUM.
DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112 IG-Like.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252P1C2 CRC64;

Query Match 27.6%; Score 454; DB 1; Length 122;
Best Local Similarity 71.5%; Pred. No. 2.1e-26;
Matches 88; Conservative 15; Mismatches 18; Indels 2; Gaps 2;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYWMVWRQAPGKLEWVANIKODGSEKYYV 100
ID HV33_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02046; M3HWE.
DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.

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DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN
[1]
RP MEDLINE=77070269; PubMed=826475;
RA Pongtong H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RL Hoppe-seyler's Z. Physiol. Chem. 357:1571-1604(1976).
[2]
RN
RP DISULFIDE BOND.
MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IgG1 MYELOMA
CC PROTEIN.
CC
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A91668; GIHUNI.
DR HSSP: P01772; 2P84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR InterPro: IPR003596; Ig-V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E5E165B CRC64;

Query Match 26.2%; Score 430.5; DB 1; Length 119;
Best Local Similarity 68.3%; Pred. No. 1e-24;
Matches 84; Conservative 17; Mismatches 17; Indels 5; Gaps 2;

OY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWROAPGKLEWVANIKODGSEKYYV 100
DB 2 VOLVSGGGVQPGSLRLSCAASGFTFSRTTHVRCAPKGLGVAVMSYBGBKHYYA 61
OY 101 DSVKGRFTISRDNAKNSLYLQMSISRAEDTAVYVCARDLKYKSSSGMPDPWGRTTYT 160
DB 62 DSVKGRFTISRDNSKNTLYLMNMSLRPEDTAVYVCAR----IRDTAM-FFAHWGSGTLVT 116
OY 161 VSS 163
DB 117 VSS 119

RESULT 10
H3F_HUMAN
ID HV3F_HUMAN STANDARD: PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;

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RN
[1]
RP MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02052; M3HUGA.
DR HSSP: P01772; 2P84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR InterPro: IPR003596; Ig-V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 26.1%; Score 429; DB 1; Length 122;
Best Local Similarity 65.0%; Pred. No. 1.4e-24;
Matches 80; Conservative 23; Mismatches 18; Indels 2; Gaps 2;

OY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWROAPGKLEWVANIKODGSEKYYV 100
DB 2 VLVZVSGGAVZPGSLRLSCAASGFTSTYIMHVRAPGKGLMLSTISYBGBBZYIA 61
OY 101 DSVKGRFTISRDNAKNSLYLQMSISRAEDTAVYVCARDLKYKSSSGMPDPWGRTTYT 160
DB 62 ASVKGRFTISRBBSKBTYLMENSLRAEDTAVYVCARGIAL-GSVAG-TDYWGSGTLVT 119
OY 161 VSS 163
DB 120 ISS 122

RESULT 11
H3F_HUMAN
ID HV3F_HUMAN STANDARD: PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RP MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; A2H0BU.
DR HSSP: P01789; 1MCP.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR InterPro: IPR003596; Ig-V.

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DR Pfam: PF00047; Ig, 1.  
 DR SMART: SM00406; IGV, 1.  
 DR PROSITE: PS50835; IG-LIKE, 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 111  
 FT NON\_TER 115 115 IG-LIKE.  
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;  
 Query Match 26.0%; Score 427.5; DB 1; Length 115;  
 Best Local Similarity 68.3%; Pred. No. 1.6e-24;  
 Matches 84; Conservative 17; Mismatches 13; Indels 9; Gaps 2;  
 QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKGLEWVANIKQDSEKYYV 100  
 DB 2 VOLVERGGGLIQPGSLRLSCAASGFTVSBMSWVRQAPGKALZWVSALYRGGT-TYYA 60  
 QY 101 DSVKGRFTISRDNKASLYLQNSLRLEADTAVYYCARDLKVKGSSGMPDPRGRTYV 160  
 DB 61 DSVKGRFTISRDRSRRTYVLYQMSLRLEADTAVYYCARDLAAR-----LFGKTTYV 112  
 QY 161 VSS 163  
 DB 113 VSS 115  
 RESULT 12  
 HV16\_MOUSE STANDARD; PRT; 136 AA.  
 ID HV16\_MOUSE  
 AC P01783;  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NpB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 RN [2]  
 RP SEQUENCE OF 17-136.  
 RX MEDLINE=77100368; PubMed=401950;  
 RA Adelung K., Milstein C., Secher D.S.;  
 RT "Molecular analysis of spontaneous somatic mutants.";  
 RL Nature 265:299-304(1977).  
 CC CC  
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 CC -----  
 DR EMBL: J00522; AAD15290.1; -  
 DR PIR: E90809; GIMS21.  
 DR PDB: 1IGC; 03-JUN-95.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig, 1.  
 DR SMART: SM00406; IGV, 1.  
 DR PROSITE: PS50835; IG-LIKE, 1.  
 KW Immunoglobulin V region; Signal; 3D-structure.  
 FT NON\_TER 1 16  
 FT SIGNAL 17 136  
 CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.

FT DOMAIN 115 119 D SEGMENT.  
 FT DOMAIN 120 136 JH4 SEGMENT.  
 FT DISULFID 38 112  
 FT CONFLICT 75 78 HYAD -> DYAD (IN REF. 2).  
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).  
 FT CONFLICT 115 115 W -> H (IN REF. 2).  
 FT CONFLICT 120 120 Y -> W (IN REF. 2).  
 FT NON\_TER 136 136  
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;  
 Query Match 26.0%; Score 427; DB 1; Length 136;  
 Best Local Similarity 66.2%; Pred. No. 2.1e-24;  
 Matches 86; Conservative 10; Mismatches 16; Indels 18; Gaps 2;  
 QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKGLEWVANIKQDSEKYYV 100  
 DB 18 VOLVESGGGLVPGGSLRLSCAASGFTFSFGHNWVRQAPGKLEWVAIVSSGSLHYA 77  
 QY 101 DSVKGRFTISRDNKASLYLQNSLRLEADTAVYYCARDLKVKGSSGMPDPRGRTYV 160  
 DB 78 DSVKGRFTISRDNKNTFLQMTSLRSEDTAVYYCAR-----WGNPYRYAMDYW 126  
 QY 154 GRTTYVSS 163  
 DB 127 GQSTVTVSS 136  
 RESULT 13  
 HV3D\_HUMAN STANDARD; PRT; 115 AA.  
 ID HV3D\_HUMAN  
 AC P01765;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-TII region TIL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78005528; PubMed=409716;  
 RA Wang A.-C., Wang I.Y., Fudenberg H.H.;  
 RT "Immunoglobulin structure and genetics. Identity between variable  
 RT regions of a mu and a gamma2 chain.";  
 RL J. Biol. Chem. 252:7192-7199(1977).  
 CC CC  
 CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS  
 CC OF IGM AND IG22 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL  
 CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO  
 CC IDENTICAL.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A02048; H3HUTL.  
 DR HSP: P01772; 2F84.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; P:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig, 1.  
 DR SMART: SM00406; IGV, 1.  
 DR PROSITE: PS50835; IG-LIKE, 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 108  
 FT NON\_TER 115 115 IG-LIKE.  
 SQ SEQUENCE 115 AA; 12356 MW; 4DC67D179F62326 CRC64;  
 Query Match 25.5%; Score 418.5; DB 1; Length 115;  
 Best Local Similarity 69.4%; Pred. No. 7.3e-24;  
 Matches 86; Conservative 12; Mismatches 15; Indels 11; Gaps 3;  
 QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKLEWVANIKQDSEKYYV 100  
 DB 111 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKLEWVANIKQDSEKYYV 100



Db 2 VOLLESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZMWGAIZGLSVSZSYA 61  
QY 101 DSVKGRFTISRDNKNSLYLQMNLSLRADPTAVYYCARDLKKVKS--SSGWFDPMGRTTV 159  
Db 62 BSKVGRFTISRDNKNSLT---MNSLRADPTAVYYCA-----KGVSAIYFBYWGZGTLV 111  
QY 160 TVSS 163  
Db 112 TVSS 115

RESULT 14  
HV18\_MOUSE  
ID HV18\_MOUSE STANDARD; PRT; 123 AA.  
AC P01787;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE (TEPC 15).  
RX MEDLINE=76222762; PubMed=819932;  
RA Rudikoff S., Potter M.;  
RT "Size differences among immunoglobulin heavy chains from  
RT phosphorylcholine-binding proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).  
RN [2]  
RP SEQUENCE FROM N.A. (H107).  
RX MEDLINE=80199926; PubMed=6769593;  
RA Early P., Huang H., Davis M., Calame K., Hood L.;  
RT "An immunoglobulin heavy chain variable region gene is generated from  
RT three segments of DNA: VH, D and JH.";  
RL Cell 19:981-992(1980).  
RN [3]  
RP SEQUENCE (S107).  
RX MEDLINE=76110488; PubMed=813561;  
RA Rudikoff S., Barstad P., Potter M., Hood L.;  
RL Unpublished results, cited by:  
RL Hood L., Campbell J.H., Elgin S.C.R.;  
RL Annu. Rev. Genet. 9:305-353(1975).  
RN [4]  
RP SEQUENCE (HPCM1, HPCM2 AND HPCM3).  
RX MEDLINE=81197602; PubMed=7231520;  
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
RT "IgG antibodies to phosphorylcholine exhibit more diversity than  
RT their IgM counterparts.";  
RL Nature 291:29-34(1981).  
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.  
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MELDOMA AND  
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A93804; AVMST5.  
DR HSSP: P01789; IMCP.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 114 IG-LIKE.  
FT NON\_TER 123  
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 25.5%; Score 418.5; DB 1; Length 123;  
Best Local Similarity 66.4%; Pred. No. 7.9e-24;  
Matches 83; Conservative 14; Mismatches 23; Indels 5; Gaps 2;

QY 41 VOLVESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZMWGAIZGLSVSZSYA 61

Db 2 VKLVESSGGGLVOPGSGRLSCATSGFTFSSDYEMWVRQAPGKRLZEMJLAASRNKANDYTE 61  
QY 99 YVDSVGRFTISRDNKNSLYLQMNLSLRADPTAVYYCARDLKKVKS--SSGWFDPMGRTTV 158  
Db 62 YSASVGRFTISRDNKNSLT---MNSLRADPTAVYYCA-----KGVSAIYFBYWGZGTLV 111  
QY 159 TVSS 163  
Db 119 TVSS 123

RESULT 15  
HV3M\_HUMAN  
ID HV3M\_HUMAN STANDARD; PRT; 119 AA.  
AC P01774;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region POM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75046755; PubMed=4139708;  
RA Capra J.D., Kehoe J.M.;  
RT "Structure of antibodies with shared idiotypic: the complete sequence  
RT of the heavy chain variable regions of two immunoglobulin M  
RT anti-gamma globulins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA  
CC GLOBULIN ACTIVITY.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A02057; M3HUPM.  
DR HSSP: P01772; 2FB4.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 112 IG-LIKE.  
FT VARIANT 54 54 N -> D (PROBABLY DUE TO DEAMINATION  
FT DURING ISOLATION).  
FT NON\_TER 119 119  
SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;

Query Match 25.5%; Score 418; DB 1; Length 119;  
Best Local Similarity 68.9%; Pred. No. 8.3e-24;  
Matches 84; Conservative 17; Mismatches 15; Indels 6; Gaps 2;

QY 41 VOLVESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZMWGAIZGLSVSZSYA 61  
Db 2 VKLVESSGGGLVOPGSGRLSCATSGFTFSSDYEMWVRQAPGKRLZEMJLAASRNKANDYTE 61  
QY 101 DSVKGRFTISRDNKNSLYLQMNLSLRADPTAVYYCARDLKKVKS--SSGWFDPMGRTTV 158  
Db 62 DSVKGRFTISRDNKNSLT---MNSLRADPTAVYYCA-----KGVSAIYFBYWGZGTLV 111  
QY 159 VT 160  
Db 118 VT 119

Search completed: September 22, 2003, 15:13:48  
Job time : 11.7293 secs



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OW protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 50.9388 Seconds  
(without alignments)  
1580.572 Million cell updates/sec

Title: US-10-052-798-10  
Perfect score: 1642  
Sequence: 1 MTMTTPSGAFLEIFNVKRL.....HHGAPQKLSIEDLNCAA 312

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	913	55.6	298	11 Q9QYF0	Q9qyf0 mus musculu
2	599.5	36.5	241	11 Q921A6	Q921a6 mus musculu
3	552	33.6	107	4 Q9NSD6	Q9nsd6 homo sapien
4	521	31.7	471	4 Q8TC77	Q8tc77 homo sapien
5	500.5	30.5	613	4 Q8WUK1	Q8wuk1 homo sapien
6	496	30.2	218	11 Q925L1	Q925l1 mus musculu
7	495	30.1	95	4 Q9ULB6	Q9ulb6 homo sapien
8	494.5	30.1	113	4 Q9UL90	Q9ul90 homo sapien
9	481	29.3	118	4 Q9UL91	Q9ul91 homo sapien
10	479	29.2	487	11 Q99KA4	Q99ka4 mus musculu
11	476	29.0	597	4 Q96B89	Q96b89 homo sapien
12	468.5	28.5	116	4 Q9UL93	Q9ul93 homo sapien
13	466	28.4	494	4 Q96K68	Q96k68 homo sapien
14	463.5	28.2	499	4 Q8NSK4	Q8nsk4 homo sapien
15	461	28.1	122	4 Q9UL84	Q9ul84 homo sapien
16	459.5	28.0	121	4 Q9UL71	Q9ul71 homo sapien

ALIGNMENTS

17	455	27.7	573	4 Q8WU38	Q8wu38 homo sapien
18	452	27.5	147	4 Q9Y509	Q9y509 homo sapien
19	447.5	27.3	479	11 Q91WP5	Q91wp5 mus musculu
20	445.5	27.1	473	11 Q91Z05	Q91z05 mus musculu
21	445	27.1	118	4 Q9UL72	Q9ul72 homo sapien
22	442.5	26.9	486	11 Q91Z07	Q91z07 mus musculu
23	441	26.9	112	4 Q9HC1	Q9hcc1 homo sapien
24	437.5	26.6	119	11 Q920E7	Q920e7 mus musculu
25	435.5	26.5	493	4 Q8NCL6	Q8ncl6 homo sapien
26	434	26.4	233	4 Q8TRC9	Q8trc9 homo sapien
27	427.5	26.0	480	11 Q91XE1	Q91xe1 mus musculu
28	426.5	26.0	131	4 Q9UL88	Q9ul88 homo sapien
29	424.5	25.9	521	4 Q8N4Y9	Q8n4y9 homo sapien
30	421.5	25.7	469	11 Q8R3V9	Q8r3v9 mus musculu
31	418	25.5	233	4 Q8NSF4	Q8nsf4 homo sapien
32	409	24.9	484	11 Q8VEA0	Q8vea0 mus musculu
33	394.5	24.0	437	11 Q9R1A4	Q9r1a4 mus musculu
34	381.5	23.2	234	4 Q8N355	Q8n355 homo sapien
35	371.5	22.6	107	4 Q9UL82	Q9ul82 homo sapien
36	366	22.3	124	6 Q9NOM4	Q9n0w4 oryctolaqus
37	363	22.1	124	6 Q9NOM6	Q9n0w6 oryctolaqus
38	363	22.1	237	4 Q8WUK4	Q8wuk4 homo sapien
39	362	22.0	124	4 Q9UL92	Q9ul92 homo sapien
40	357.5	21.8	104	4 Q9UL87	Q9ul87 homo sapien
41	351.5	21.4	112	4 Q9UGP3	Q9ugp3 homo sapien
42	350	21.3	237	4 Q8WU6	Q8wut6 homo sapien
43	346.5	21.1	236	4 Q96E61	Q96e61 homo sapien
44	338.5	20.6	119	4 Q9UL94	Q9ul94 homo sapien
45	338	20.6	159	4 Q96Q50	Q96q50 homo sapien

RESULT 1

ID	Q9QYF0	PRELIMINARY:	PRT:	298 AA.
AC	Q9QYF0:	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	CN 8 scfv.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Balb/c; TISSUE=Spleen;			
RX	MEDLINE=20183931; PubMed=10706631;			
RA	Shinozuka N., Demura T., Fukuda H.;			
RT	"Isolation of a vascular cell wall-specific monoclonal antibody			
RT	recognizing a cell polarity by using a phage display subtraction			
RT	method."			
RU	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).			
DR	EMBL: AB036341; BAA8633.1; .			
DR	HSSP: P01607; IRET.			
DR	InterPro: IPR007110; Ig-1-like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig-V.			
DR	Pfam: PF00047; Ig_2.			
DR	SMART: SM00406; IGV_2.			
DR	PROSITE: PS50835; IG_LIKE; 2.			
DR	PROSITE: PS50835; IG_LIKE; 2.			
DR	SEQUENCE 298 AA: 31867 MW; EDP9658A17004317 CRC64;			

Query Match 55.6%; Score 913; DB 11; Length 298;

Best Local Similarity 62.8%; Pred. No. 5.9e-63;

Matches 186; Conservative 25; Mismatches 65; Indels 20; Gaps 5;

OY 1 MTMTTPSGAFLEIFNVKRLFAIPLVPPYAPAPAMAGVOLVESGGGLVPGGSLRLS 60  
Db 1 MTMTTPSGAFLEIFNVKRLFAIPLVPPYAPAPAMAGVOLVESGGGLVPGGSLRLS 60

```

QY 61 CAAGFTTSSYWMVROAPGKLEWVANIKODGSEKYYVDSYKGFITISRDNAKSLYL 120
DB 61 CAAGSDFSRKYMVMVROAPGKLEWIGEIFINPDSSITINTYPSLKDFITISRDNAKSLYL 120
QY 121 QMNSLRAREFTANYCARDLKVKSGSGFDPWGKGTITYVSSGGSGSGSGSGSGSS- 179
DB 121 QMSKYRSEDTALYCAR-----ASYGHSAYWGGQTYTVSSGGSGSGSGSGSGSDI 174
QY 180 ELTODPA-VSYALGOTVRITTCOGDSLRSYASMYOOPGQAPVLVYIGKNNRPSGIPDRF 238
DB 175 ELTGPASISASVGETVITTCASGNINHYLAWYQOKQKSQLLVYNAKTLADGVPSEF 234
QY 239 GSSSGNTASTLTITGAQAEDEADYYCNSRDSGNN-----VYFGGCTKLTVLGAA 289
DB 235 GSGSGGTGYSLKINSIQPEDFGSYC-----QHFWTPTYTFEGGCTKLKIRAA 283

RESULT 2
Q921A6 PRELIMINARY: PRT: 241 AA.
ID Q921A6;
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98170165; Pubmed=9509426;
RX Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL: U88067; AA848044.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IgV; 2.
DR PROSITE: PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 36.5%; Score 599.5; DB 11; Length 241;
Best Local Similarity 51.4%; Pred. No. 9,3e-39;
Matches 128; Conservative 35; Mismatches 65; Indels 21; Gaps 7;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVROAPGKLEWVANIKODGSKYYV 100
DB 2 VKLQGGPELKRPGEVTKISCAAGTYFTDYGNMVAQKAPGKLMWGINITYTGEPYA 61
QY 101 DSVKGFRTISRDNAKSLYLMNLSRAEDTAVYYCAR-DLTKVKGSSSGMFPDWPWGCTTV 159
DB 62 DDFKGFRTISRDNAKSLYLMNLSRAEDTAVYYCAR-DLTKVKGSSSGMFPDWPWGCTTV 114
QY 160 TVSSGGSGSGSGSGSGSGSS-ELTODP-AVSVALGOTVRITTCOGDSLRSYASMYOOPG 217
DB 115 TVSSGGSGSGSGSGSGSGSDIELTPSSLSASLSGKVTITTCASODINKIYAWYQKRG 174
QY 218 QAP-----VLYYIGKNNRPSGIPDRSGSSSGNTASTLTITGAQAEDEADYYCNSRDSGNN 273
DB 175 KQPRSAHTLHYIQ---PGIPSRFSGSGSGSDYSPSISNLBEDIATYYCLAHYD---NL 227
QY 274 VYFGGCTKL 282
DB 228 HTFGGCTKL 236

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RESULT 3
Q9NSD6 PRELIMINARY: PRT: 107 AA.
ID Q9NSD6;
AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Lymphocytes;
RA Hermann A.;
RT "Autoimmunity.";
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL: I43092; AAA69746.2; -.
DR HSSP: P01709; 2MCG.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 33.6%; Score 552; DB 4; Length 107;
Best Local Similarity 38.1%; Pred. No. 1.6e-35;
Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 180 ELTODPAVSVALGOTVRITTCOGDSLRSYASMYOOPGQAPVLVYIGKNNRPSGIPDRS 239
DB 1 ELTODPVSVALGOTVRITTCOGDSLRSYASMYOOPGQAPVLVYIGKNNRPSGIPDRS 60
QY 240 GSSSGNTASTLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 286
DB 61 GSSSGNTASTLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 107

RESULT 4
Q8TC77 PRELIMINARY: PRT: 471 AA.
ID Q8TC77;
AC 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Spleen;
RA Strausberg R.;
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC024289; AA824289.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

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OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/Genbank/DDJ databases.
DR EMBL: AB035268; BAA87067.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match
Best Local Similarity 30.1%; Score 495; DB 4; Length 95;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMWVROAPGKGLVWVNIKODGSEKYYV 100
DB 1 VOLVESGGGLVPGGSLRLSCAASGFTSSYMWVROAPGKGLVWVNIKODGSEKYYV 60
QY 101 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYCARDLLKVGSSSGMFDWGKITYT 160
DB 61 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYC 95

RESULT 8
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035024; AAD56260.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match
Best Local Similarity 30.1%; Score 494.5; DB 4; Length 113;
Matches 97; Conservative 7; Mismatches 8; Indels 11; Gaps 1;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMWVROAPGKGLVWVNIKODGSEKYYV 100
DB 2 VOLVESGGGLVPGGSLRLSCAASGFTSSYGMHVRQAPGKGLVWVNIKODGSEKYYV 61
QY 101 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYCARDLLKVGSSSGMFDWGKITYT 160
DB 101 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYCARDLLKVGSSSGMFDWGKITYT 160

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DB 62 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYCARDLLKVGSSSGMFDWGKITYT 110
QY 161 VSS 163
DB 111 VSS 113

RESULT 9
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035023; AAD56259.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match
Best Local Similarity 29.3%; Score 481; DB 4; Length 118;
Matches 98; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMWVROAPGKGLVWVNIKODGSEKYYV 100
DB 2 VOLVESGGGLVPGGSLRLSCAASGFTSSYMNVRQAPGKGLVWVNIKODGSEKYYV 61
QY 101 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYCARDLLKVGSSSGMFDWGKITYT 160
DB 62 DSVKGRFTISRDNKNSLYLQNSLRADDTAVYYCAR-----GDSSEAFDWMGGTWT 115
QY 161 VS 162
DB 116 VS 117

RESULT 10
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;

```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Wagaitsuna M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto Y., Nakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,  
 RA Ninomiya K., Iwayanagi T.,  
 RT "NEO human cDNA sequencing project."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK027379; BAB55072.1; -  
 DR InterPro: IPR007110; Ig-Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_4.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Hypothetical protein  
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEB4C0E CRC64;

Query Match 28.4%; Score 466; DB 4; Length 494;  
 Best Local Similarity 74.8%; Pred. No. 5.3e-28;  
 Matches 92; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

OY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSVWRQAPGKGLEWVANIKDGSSEKYYV 100  
 |||||  
 DB 21 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSVWRQAPGKGLEWVANIKDGSSEKYYV 80  
 |||||  
 OY 101 DSVKGRFTISRDNANKNSLYLQNSLRADPTAVYVCARDLKVKGSSSGFDPMGKGTYYT 160  
 |||||  
 DB 81 DSVKGRFTISRDNANKNSLYLQNSLRADPTAVYVCARD--SCNGALCYGFSFGGCTLYT 138  
 |||||  
 OY 161 VSS 163  
 |||||  
 DB 139 VSS 141

RESULT 14

O8NSK4 PRELIMINARY; PRT; 499 AA.  
 AC O8NSK4;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Strausberg R.,  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC032249; AAH32249.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-Like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_4.  
 DR SMART: SM00409; Ig; 4.  
 DR SMART: SM00407; IGcl; 2.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.

SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;  
 Query Match 28.2%; Score 463.5; DB 4; Length 499;  
 Best Local Similarity 73.8%; Pred. No. 8.4e-28;  
 Matches 93; Conservative 9; Mismatches 21; Indels 3; Gaps 2;

OY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSVWRQAPGKGLEWVANIKDGSSEKYYV 100  
 |||||  
 DB 21 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSVWRQAPGKGLEWVANIKDGSSEKYYV 80  
 |||||  
 OY 101 DSVKGRFTISRDNANKNSLYLQNSLRADPTAVYVCARDLKVK--KGSSSGFDPMGKGT 157  
 |||||  
 DB 81 DSVKGRFTISRDNANKNSLYLQNSLRADPTAVYVCARDPTKCSGSGCLGTYMDYWGKGT 140  
 |||||  
 OY 158 TVTVSS 163  
 |||||  
 DB 141 TVTVSS 146

RESULT 15

O9UL84 PRELIMINARY; PRT; 122 AA.  
 AC O9UL84;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive Immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035030; AAD56266.1; -  
 DR HSP: P01772; 2F84.  
 DR InterPro: IPR007110; Ig-Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT TER 122  
 SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 28.1%; Score 461; DB 4; Length 122;  
 Best Local Similarity 75.0%; Pred. No. 2.1e-28;  
 Matches 93; Conservative 9; Mismatches 18; Indels 4; Gaps 2;

OY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSVWRQAPGKGLEWVANIKDGSSEKYYV 100  
 |||||  
 DB 2 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSVWRQAPGKGLEWVANIKDGSSEKYYV 61  
 |||||  
 OY 101 DSVKGRFTISRDNANKNSLYLQNSLRADPTAVYVCARDLKVKGSSSGFDPMGKGTYY 159  
 |||||  
 DB 62 DSVKGRFTISRDNANKNSLYLQNSLRADPTAVYVCARD--ERGLVGTFFDYWGQGLTV 118  
 |||||  
 OY 160 TVSS 163  
 |||||  
 DB 119 TVSS 122

Search completed: September 22, 2003, 15:21:24  
 Job time : 51.938 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 51.9441 Seconds

(without alignments)  
947.272 Million cell updates/sec

Title: US-10-052-798-11

Perfect score: 1638

Sequence: 1 MTWITPSCGAFLEIFNVK.....HHGAAEQKLISEEDLNCA 310

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A.GeneSeq\_19Jun03:\*

- 1: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:\*
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- 9: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:\*
- 12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:\*
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- 19: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:\*
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- 21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:\*
- 22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:\*
- 23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*
- 24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1638	100.0	310	AAW83324	Single chain Apo-2
2	1638	100.0	310	ABB09605	Amino acid sequenc
3	1638	100.0	310	ABG74386	Single chain antib
4	1231.5	75.2	309	AAW83322	Single chain Apo-2
5	1231.5	75.2	309	ABB09603	Amino acid sequenc
6	1231.5	75.2	309	ABG74384	Single chain antib
7	1231	75.2	312	AAW83323	Single chain Apo-2
8	1231	75.2	312	ABB09604	Amino acid sequenc
9	1231	75.2	312	ABG74385	Single chain antib

10	1108.5	67.7	252	23	ABP45508	Human Blys binding
11	1089.5	66.5	252	23	ABP44977	Human Blys binding
12	1087.5	66.4	252	23	ABP45190	Human Blys binding
13	1075.5	65.7	246	21	AAV58235	Internalising anti
14	1071	65.4	243	23	ABP45938	Human Blys binding
15	1064.5	65.0	248	23	ABP45879	Human Blys binding
16	1063	64.9	247	23	ABP45942	Human Blys binding
17	1053.5	64.3	258	23	ABP45830	Human Blys binding
18	1050.5	64.1	260	23	ABP45447	Human Blys binding
19	1048.5	64.0	256	23	ABP44828	Human Blys binding
20	1046.5	63.9	250	23	ABP45450	Human Blys binding
21	1045.5	63.8	252	23	ABP45351	Human Blys binding
22	1045.5	63.8	254	23	ABP44970	Human Blys binding
23	1035.5	63.2	250	23	ABP45409	Human Blys binding
24	1033	63.1	304	22	AA63634	Amino acid sequenc
25	1031	62.9	251	23	ABP45298	Human Blys binding
26	1030.5	62.9	252	23	ABP45616	Human Blys binding
27	1028.5	62.8	614	23	ABB06275	Plasmd scfv(CC046
28	1027.5	62.7	254	23	ABP44972	Human Blys binding
29	1027	62.7	247	23	ABP46081	Human Blys binding
30	1027	62.7	251	23	ABP45531	Human Blys binding
31	1027	62.7	304	22	AA63639	Amino acid sequenc
32	1026	62.6	251	23	ABP45400	Human Blys binding
33	1024	62.5	253	23	ABP44847	Human Blys binding
34	1023.5	62.5	254	23	ABP45748	Human Blys binding
35	1023	62.5	251	23	ABP44944	Human Blys binding
36	1021.5	62.4	254	23	ABP44870	Human Blys binding
37	1021	62.3	247	23	ABP45881	Human Blys binding
38	1021	62.3	247	23	ABP45967	Human Blys binding
39	1020	62.3	251	23	ABP45321	Human Blys binding
40	1018	62.1	246	23	ABP45945	Human Blys binding
41	1017.5	62.1	245	24	ABJ19834	Human VEGF-2 relat
42	1016	62.0	253	23	ABP45189	Human Blys binding
43	1015.5	62.0	259	22	ABP45603	Huntingtin Intrabo
44	1015.5	62.0	252	23	ABP44945	Human Blys binding
45	1013	61.8	253	24	ABJ19830	Human VEGF-2 relat

#### ALIGNMENTS

RESULT 1		AAW83324 strand; Protein: 310 AA.
ID	AAW83324	
XX	AAW83324:	
AC		
XX		
DT	16-MAR-1999 (first entry)	
XX		
DE	Single chain Apo-2 antibody 24c4.	
XX		
KW	Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;	
KW	tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;	
XX	TNF cytokine.	
OS	Homo sapiens.	
XX		
PN	WO9851793-A1.	
XX		
PD	19-NOV-1998.	
XX		
PF	14-MAY-1998; 98WO-US09704.	
XX		
PR	09-FEB-1998; 98US-0020746.	
XX		
PA	15-MAY-1997; 97US-0857216.	
XX		
PI	(GETH ) GENENTECH INC.	
XX		
DR	Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;	
XX	WPI; 1999-045228/04.	
XX	N-PSDB; AAV72534.	

PT Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

CC The present invention describes human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2; useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification. The present  
 CC sequence represents a single chain Apo-2 antibody, designated 24c4.  
 XX

SQ Sequence 310 AA:

Query Match 100.0%; Score 1638; DB 20; Length 310;

Best Local Similarity 100.0%; Pred. No. 3.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTIPSEGAFFLEIFNVKLLFAIPLVVPEFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60  
 DB 1 MTMTIPSEGAFFLEIFNVKLLFAIPLVVPEFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60  
 QY 61 CAASGFIFSSYGMHWVROAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
 DB 61 CAASGFIFSSYGMHWVROAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
 QY 121 QNNSLRAEPTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSQSVLTQPP 180  
 DB 121 QNNSLRAEPTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSQSVLTQPP 180  
 QY 181 SVSGAPGQGVITISCTGRSSNIGAGHDVHYQQLPCTAPKLLTYDSDNRPSSGVPDRFSSGR 240  
 DB 181 SVSGAPGQGVITISCTGRSSNIGAGHDVHYQQLPCTAPKLLTYDSDNRPSSGVPDRFSSGR 240  
 QY 241 SGTASLATITGLQAEDEADYQCQSDSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300  
 DB 241 SGTASLATITGLQAEDEADYQCQSDSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300  
 QY 301 ISEEDLNGAA 310  
 DB 301 ISEEDLNGAA 310  
 RESULT 2  
 ID ABB09605 standard; Protein: 310 AA.  
 XX ABB09605;  
 AC  
 XX  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Amino acid sequence of single-chain Apo-2 antibody 24c4.  
 XX  
 XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
 KM caspase; apoptosis; cancer; antibody.  
 XX  
 OS Bacteriophage.

XX US6342369-B1.  
 PN  
 XX  
 PD 29-JAN-2002.  
 XX  
 XX  
 PF 14-MAY-1998; 98US-0079029.  
 XX

XX 15-MAY-1997; 97US-046615P.  
 PR 09-FEB-1998; 98US-074119P.  
 XX

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ;

PI WPI; 2002-224941/28.  
 XX  
 DR N-PSDB; ABL41735.  
 XX

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or  
 PT stimulating apoptosis in cancer cells, thus especially useful in the  
 PT treatment of cancer, or in enhancing immune-mediated cell death

XX Example 14; Fig 16; 63pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated  
 CC 24c4, which is isolated from a phage library. It is believed that  
 CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)  
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent  
 CC apoptosis and activating nuclear factor-kappa B. A soluble  
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2  
 CC antibodies may be used to activate or stimulate apoptosis in cancer  
 CC cells. They are therefore especially useful in the treatment of cancer,  
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to  
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in  
 CC affinity purification of Apo-2 from recombinant cell culture or natural  
 CC sources.  
 XX

SQ Sequence 310 AA:

Query Match 100.0%; Score 1638; DB 23; Length 310;

Best Local Similarity 100.0%; Pred. No. 3.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTIPSEGAFFLEIFNVKLLFAIPLVVPEFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60  
 DB 1 MTMTIPSEGAFFLEIFNVKLLFAIPLVVPEFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60  
 QY 61 CAASGFIFSSYGMHWVROAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
 DB 61 CAASGFIFSSYGMHWVROAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
 QY 121 QNNSLRAEPTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSQSVLTQPP 180  
 DB 121 QNNSLRAEPTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSQSVLTQPP 180  
 QY 181 SVSGAPGQGVITISCTGRSSNIGAGHDVHYQQLPCTAPKLLTYDSDNRPSSGVPDRFSSGR 240  
 DB 181 SVSGAPGQGVITISCTGRSSNIGAGHDVHYQQLPCTAPKLLTYDSDNRPSSGVPDRFSSGR 240  
 QY 241 SGTASLATITGLQAEDEADYQCQSDSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300  
 DB 241 SGTASLATITGLQAEDEADYQCQSDSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300  
 QY 301 ISEEDLNGAA 310  
 DB 301 ISEEDLNGAA 310  
 RESULT 3  
 ID ABB74386 standard; Protein: 310 AA.  
 XX ABB74386;  
 AC  
 XX  
 XX

DT 11-APR-2003 (first entry)  
 XX Single chain antibody (scfv) fragment 24C4.  
 DE  
 XX  
 KW Apo-2; tumour necrosis factor family; TNFR; gene therapy;  
 KW apoptosis; tissue-specific typing; affinity purification;  
 KW competitive-type receptor binding assay; mouse; 24C4.  
 XX  
 OS Mus sp.  
 XX  
 PN US2002150985-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 02-NOV-2001; 2001US-0052798.  
 XX  
 PR 15-MAY-1997; 97US-046615P.  
 PR 09-FEB-1998; 98US-074119P.  
 PR 14-MAY-1998; 98US-0079029.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
 XX  
 DR WPI; 2003-198287/19.  
 DR N-PSDB; ABX16409.  
 XX  
 PT New Apo-2 polypeptides and polynucleotides, useful for inducing  
 PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in  
 PT quantitative diagnostic assays, or in generating antibodies against  
 PT Apo-2 -  
 XX  
 PS Example 14; Fig 16; 64pp; English.  
 XX  
 CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2  
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo  
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control  
 CC against samples containing unknown quantities of Apo-2, in generating  
 CC antibodies, in affinity purification techniques, and in competitive-type  
 CC receptor binding assays when labelled with, for instance, radiolodine,  
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
 CC diagnostic for tissue-specific typing. This is the amino acid sequence  
 CC of the single chain antibody fragment (svfv) 24C4 used in the  
 CC preparation of anti-apo-2 antibodies.  
 CC  
 XX Sequence 310 AA;  
 SO  
 Query Match 100.0%; Score 1638; DB 24; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 3,7e-103;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTTPSGAFLEIFNNKLLFAIPLVPPYAAQVQVLOSOGGVQPGRSRLS 60  
 DB 1 MTMTTPSGAFLEIFNNKLLFAIPLVPPYAAQVQVLOSOGGVQPGRSRLS 60  
 QY 61 CAASGEFTSSYGMHWROAPKGLWVAGIFYDGGNKRYADSVKGRFTISDNRNTLYL 120  
 DB 61 CAASGEFTSSYGMHWROAPKGLWVAGIFYDGGNKRYADSVKGRFTISDNRNTLYL 120  
 QY 121 QMNSLRAEDTAIVVYCCARDRGYYMDVWKGTTVTYSSGGSGSGGGSQSVLTQPP 180  
 DB 121 QMNSLRAEDTAIVVYCCARDRGYYMDVWKGTTVTYSSGGSGSGGGSQSVLTQPP 180  
 QY 181 SVSAPGQRTVITCTGRSSNIGAGHDVWYQOLPGTAKLLIYDSSNRPSPVPFRSSSR 240  
 DB 181 SVSAPGQRTVITCTGRSSNIGAGHDVWYQOLPGTAKLLIYDSSNRPSPVPFRSSSR 240  
 QY 241 SGTASALATITGLQAEDEADYYCQSYDSSLRGSVFGGKRYTVLGAHHHHHGAAEQKL 300  
 DB 241 SGTASALATITGLQAEDEADYYCQSYDSSLRGSVFGGKRYTVLGAHHHHHGAAEQKL 300  
 QY 301 ISEEDLNGAA 310  
 DB 301 ISEEDLNGAA 310

DB 301 ISEEDLNGAA 310  
 RESULT 4  
 AAW83322  
 ID AAW83322 standard; Protein; 309 AA.  
 XX  
 XX AAW83322;  
 AC  
 XX 16-MAR-1999 (first entry)  
 DT  
 XX  
 DE Single chain Apo-2 antibody 16E2.  
 KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
 KW TNF cytokine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9851793-A1.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 14-MAY-1998; 98WO-US09704.  
 XX  
 PR 09-FEB-1998; 98US-0020746.  
 PR 15-MAY-1997; 97US-0857216.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
 XX  
 DR WPI; 1999-045228/04.  
 DR N-PSDB; AAV72532.  
 XX  
 CC Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 CC conditions linked with decreased apoptosis e.g. cancer, and produce  
 CC antibodies to increase or decrease apoptosis  
 CC  
 XX Example 14; Fig 16; 134pp; English.  
 PS  
 CC The present invention describes human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification. The present  
 CC sequence represents a single chain Apo-2 antibody, designated 16E2.  
 CC  
 XX Sequence 309 AA;  
 SO  
 Query Match 75.2%; Score 1231.5; DB 20; Length 309;  
 Best Local Similarity 78.0%; Pred. No. 1.1e-75;  
 Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTTPSGAFLEIFNNKLLFAIPLVPPYAAQVQVLOSOGGVQPGRSRLS 60  
 DB 1 MTMTTPSGAFLEIFNNKLLFAIPLVPPYAAQVQVLOSOGGVQPGRSRLS 60

QY	61	CAASGTFSSYGHHWRQAQPKGLKEMVAGIFPDGKNKYAAQSVGRFTISDNKNTLYL	120
Db	61	CASGTFPDYDGSMWRQAPKGLEMGVSGIMNGSISTGYADSVAGRATISDNANKNLTLYL	120
QY	121	QMSLSRAEDPTAYYYCAR---DRGYIYNDWMCKGTYYYVSSGGGGSGGGGGSGGSQSYLV	176
		: : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	121	QMNSLAEDPTAYYYCAKILIGACRGWYF-DLMCKGTYYYVSSGGGGSGGGGGSGGS-SEL	178
QY	177	TOPPSYSAQGORVTISCTGRSSNTGAGHDHWYOOLPCTPAKLIIYDDSNRPSPGVDRF	236
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	179	TODPASVALGCVTRITCGDSLR--STYSMWYOQAFQAPVLVIITGKKNRPSGLIDRF	235
QY	237	SGSRGSTASLIATLGIAEADADYYCQSDYSLRSGVFGGCTKYTVLGAANHHNNHGA	296
		: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	236	SGSSSGNTFASLITFGAODEADADYYCNRSRDSGNHYVGCGTKTLVGAANHHNNHGA	295
QY	297	EOKLISEEDLNCAA 310	
Db	296	EOKLISEEDLNCAA 309	

RESULTS	
ABB09603	
ID	ABB09603 standard; Protein: 309 AA
XX	
AC	ABB09603;
XX	
DT	29-MAY-2002 (first entry)

**Amino acid sequence of single-chain Apo-2 antibody 16E2.**

KM Human, Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
KW caspase; apoptosis; cancer; antibody.

OS Bacteriophage.

PN US6342369-B1.

PD 29-JAN-2002.

14-MAY-1998; 98US-0079029.

PR	15-MAY-1997;	97US-046615P.
DD	08-FEB-1998;	98HC-074110D

XX  
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DA (CEFH ) GENENMECH INC

XX  
XX  
PT    Aschkenazi A.T.

XX  
DR WPT: 2002-224941/28

DR N-PSDB; ABL41/33.  
XX

PT stimulating apoptosis in cancer cells, thus especially useful in the

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Example 14, Fig 10, 00pp, English

16E2, which is isolated from a phage library. It is believed that

family. Apo-2 polypeptide is capable of triggering caspase-dependent

extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L).

CC cells. They are therefore especially useful in the treatment of

detect expression of Apo-2 in specific cells, tissues or serum, and in

cc sources.

**SQ Sequence 309 AA;**

Query Match	75.2%;	Score 1231.5;	DB 23;	Length 309;
Best Local Similarity	78.0%;	Pred. No. 1.1e-75;		
Matches 245;	Conservative 20;	Mismatches 40;	Indels 9;	Gaps 4;

OY	MMITPSPGAEFLFEINVKKLLFALRPLVPEFAAPRAAOVOLVOSGGVPOPRSLRS	60
OY	MMITPSPGAEFLFEINVKKLLFALRPLVPEFAAPRAAOVOLVOSGGVPOPRSLRS	60
Dd	1 MMITPSPGAEFLFEINVKKLLFALRPLVPEFAAPRAAOVOLVOSGGVPOPRSLRS	60
OY	61 CAASGFLFSSYGNHWVRQAPKGLEWAGLFDGNGNKTYADSVKRGFTISDNKNTLYL	120
Dd	61 CAASGFLFDYDYGHSWVRQAPKGLEWAGLFDGNGNKTYADSVKRGFTISDNKNTLYL	120
OY	121 QMSLSLAEDPLAVYYCAR---DRGYUUDMVMGKSTTVTVSSGGSGSGSGSGSGSOVL	176
Dd	121 QMSLSLAEDPLAVYYCAKLLGAGRGWTF-DLMCKGTTTVTVSSGGSGSGSGSGSGSGS-SEL	178
OY	177 TOPPSVSGARQAVTISCTGRSSNTGAGNDVNTYQQLFETAPKLLIYDSSNRSPGVDRF	236
Dd	179 TOPPAVSVALGQGVVTRITCGDSLR--SYVASWYQAKRQAPVLYTGKNNRPSGLIDRF	235
OY	237 SSGRSSTASLATTGLQADEADAYYCOSVDSLRSVFGGCTKTVLGLAANNNHNGAA	296
Dd	236 SGGSSGNTASLTITGQADEADAYYCNSRDSGNNVPEGGKTVLGLAANNNHNGAA	295
OY	297 EOKLISEEDLNGAA 310	
Dd	296 EOKLISEEDLNGAA 309	

RESULT 6  
ABG74384  
ID ABG74384 standard; Protein; 309 AA

AC ABG74384

DT 11-APR-2003 (first entry)

DE Single chain antibody (scFv) fragment 16E2.

KW Apo-2; tumour necrosis factor family; TNFR; gene therapy; TNF; apoptosis; tissue-specific tumour; affinity purification

Abbreviation	Definition
KW	competitive-type receptor binding assay; mouse; 16E2.
XY	

05	Mus sp.
XX	

PN 052002150985-A1  
XX

PD 17-0031-2002  
XX

XX 02-NOV-2001; 2001US-0052/98.

PR	13-MAY-1997;	97US-040613P.
PR	09-FEB-1998;	98US-074119P.

FN 14-MAY-1956; 3603-00/3023  
XX

XX

[illegible]

DR N-PSDB; ABX16407.

PT New Apo-2 polypeptides and polynucleotides, useful for inducing

PT quantitative diagnostic assays, or in generating antibodies against

XX

[illegible]

CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo

CC against samples containing unknown quantities of Apo-2, in generating

CC antibodies, in affinity purification techniques, and in competitive-type  
 CC receptor binding assays when labelled with, for instance, radioiodine,  
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
 CC diagnostic for tissue-specific typing. This is the amino acid sequence  
 CC of the single chain antibody fragment (svf) 10E2 used in the  
 CC preparation of anti-apo-2 antibodies.

XX Sequence 309 AA;

Query Match 75.2%; Score 1231.5; DB 24; Length 309;  
 Best Local Similarity 78.0%; Pred. No. 1.1e-75;  
 Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTIPSGAFLEIFNFKLLFAIPLVPPFAAPAAQVQVLOS GGSGGVOPGRSLRLS 60  
 DB 1 MTMTIPSGAFLEIFNFKLLFAIPLVPPFAAPAAQVQVLOS GGSGGVOPGRSLRLS 60  
 QY 61 CAASGFTFSSYGMHVRQAPGKGLFWAGIFYDGKNTYADSVKGRFTISRDNKNTLYL 120  
 DB 61 CAASGFTFDDYGMVVRQAPGKGLFWAGIFYDGKNTYADSVKGRFTISRDNKNTLYL 120  
 QY 121 QMNSLRADDTAVYYCAR-----DRGYMDVMGKGTIVVSSGGSGSGSGSGSSQVYL 176  
 DB 121 QMNSLRADDTAVYYCARLGLAGRGWYF-DLMGKGTIVVSSGGSGSGSGSGSGSSQVYL 178  
 QY 177 TOPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGVPDRF 236  
 DB 179 TOPDAVSVYALGQYRITTCQDSLR---SYTASWYQQRGQAPVLVITGKNNRPSGIPDRF 235  
 QY 237 SGRSGTSASLAITGLQAEDEADYVCOYSDSLRSVFGGSKTKYVLGAANHHNHGAA 296  
 DB 236 SSSSGTSASLAITGLQAEDEADYVCOYSDSLRSVFGGSKTKYVLGAANHHNHGAA 295  
 QY 297 EOKLISEEDLNGAA 310  
 DB 296 EOKLISEEDLNGAA 309

#### RESULT 7

AAW83323  
 ID AAW83323 standard; Protein: 312 AA.

AC AAW83323;

XX 16-MAR-1999 (first entry)

DE Single chain Apo-2 antibody 20E6.

KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
 KW TNF cytokine.

XX Homo sapiens.

XX WO9851793-A1.

XX 19-NOV-1998.

XX 14-MAY-1998; 98WO-US09704.

XX 09-FEB-1998; 98US-0020746.

PR 15-MAY-1997; 97US-0857216.

XX (GETH ) GENENTECH INC.

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;

XX WPI; 1999-045228/04.

DR N-PSDB; AAV72533.

XX Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

PS The present invention describes human Apo-2. Apo-2 can be used  
 XX therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimera useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification. The present  
 CC sequence represents a single chain Apo-2 antibody, designated 20E6.

SQ Sequence 312 AA;

Query Match 75.2%; Score 1231; DB 20; Length 312;  
 Best Local Similarity 77.7%; Pred. No. 1.2e-75;  
 Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFNFKLLFAIPLVPPFAAPAAQVQVLOS GGSGGVOPGRSLRLS 60  
 DB 1 MTMTIPSGAFLEIFNFKLLFAIPLVPPFAAPAAQVQVLOS GGSGGVOPGRSLRLS 60  
 QY 61 CAASGFTFSSYGMHVRQAPGKGLFWAGIFYDGKNTYADSVKGRFTISRDNKNTLYL 120  
 DB 61 CAASGFTFSSYGMHVRQAPGKGLFWAGIFYDGKNTYADSVKGRFTISRDNKNTLYL 120  
 QY 121 QMNSLRADDTAVYYCAR-----RQYMDVMGKGTIVVSSGGSGSGSGSGSSQVYL 172  
 DB 121 QMNSLRADDTAVYYCARLGLAGRGWYF-DPMGRGTIVVSSGGSGSGSGSGSSQVYL 178  
 QY 173 QSVLTQPPSVGAPGQRYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232  
 DB 179 -SELTOPDAVSVYALGQYRITTCQDSLR---SYTASWYQQRGQAPVLVITGKNNRPSGI 234  
 QY 233 PDRTSGRSSTASLAITGLQAEDEADYVCOYSDSLRSVFGGSKTKYVLGAANHHNH 292  
 DB 235 PDRTSGRSSTASLAITGLQAEDEADYVCOYSDSLRSVFGGSKTKYVLGAANHHNH 294  
 QY 293 HGAAPQKLISEEDLNGAA 310  
 DB 295 HGAAPQKLISEEDLNGAA 312

#### RESULT 8

ABB09604  
 ID ABB09604 standard; Protein: 312 AA.

AC ABB09604;

XX 29-MAY-2002 (first entry)

DE Amino acid sequence of single-chain Apo-2 antibody 20E6.

KW Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;  
 KW caspase; apoptosis; cancer; antibody.

XX Bacteriophage.

XX US6342369-B1.

```

PD 29-JAN-2002.
XX
XX 14-MAY-1998: 98US-0079029.
XX
XX 15-MAY-1997: 97US-046615P.
XX
XX 09-FEB-1998: 98US-074119P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ;
XX
XX MPI: 2002-224941/28.
XX
XX N-PSDB; AB141734.
XX
XX New nucleic acids encoding an Apo-2 ligand, useful for activating or
XX stimulating apoptosis in cancer cells, thus especially useful in the
XX treatment of cancer, or in enhancing immune-mediated cell death -
XX
XX Example 14; Fig 16; 68pp; English.
XX
XX The present sequence represents a single-chain Apo-2 antibody, designated
XX 20E6, which is isolated from a phage library. It is believed that
XX Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
XX family. Apo-2 polypeptide is capable of triggering caspase-dependent
XX apoptosis and activating nuclear factor-kappa B. A soluble
XX extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
XX antibodies may be used to activate or stimulate apoptosis in cancer
XX cells. They are therefore especially useful in the treatment of cancer,
XX to enhance immune-mediated cell death in cells expressing Apo-2, to
XX detect expression of Apo-2 in specific cells, tissues or serum, and in
XX affinity purification of Apo-2 from recombinant cell culture or natural
XX sources.
XX
XX Sequence 312 AA:
XX
XX Query Match 75.2%; Score 1231; DB 23; Length 312;
XX Best Local Similarity 77.7%; Pred. No. 1.2e-75;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4:
XX
XX 1 MTMTPTSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVDSGGGVOPGRLRLS 60
XX 1 MTMTPTSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVDSGGGVOPGRLRLS 60
XX
XX 61 CAASGTFSSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX 61 CAASGTFSSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX
XX 121 QMNSLRAEDTAVYYCARD-----RgyyMDVMGKTTVYSSGGSGSGGSGGGS 172
XX 121 QMNSLRAEDTAVYYCARD-----RgyyMDVMGKTTVYSSGGSGSGGSGGGS 172
XX
XX 173 QSVLTQPPSVSGAPGQRTVISTGTRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSCV 232
XX 173 -SELTDQPAVSVALGQTVRITCOGDSLR---SYIASWYQOKPGQAPVLYIYKKNRPSGI 234
XX
XX 233 PRFGSGRSGTASLAITGLQAEDEADYVCOYSDSLRSGVPGGKRYVTLGAHHHHH 292
XX 233 PRFGSSSSGNTASLITITGAQAEDEADYVCOYSDSLRSGVPGGKRYVTLGAHHHHH 294
XX
XX 293 HGAAEOKLISEDLNGAA 310
XX 295 HGAAEOKLISEDLNGAA 312
XX
XX Db
XX
XX RESULT 9
XX ABG74385
XX ID ABG74385 standard; Protein; 312 AA.
XX
XX AC ABG74385;
XX
XX AC
XX
XX DT 11-APR-2003 (first entry)
XX
XX XX Single chain antibody (scFv) fragment 20E6.

```

```

XX
XX Apo-2; tumour necrosis factor family; TNFR; gene therapy;
XX apoptosis; tissue-specific typing; affinity purification;
XX competitive-type receptor binding assay; mouse; 20E6.
XX
XX Mus sp.
XX
XX US2002150985-A1.
XX
XX 17-OCT-2002.
XX
XX 02-NOV-2001: 2001US-0052798.
XX
XX 15-MAY-1997: 97US-046615P.
XX
XX 09-FEB-1998: 98US-074119P.
XX
XX 14-MAY-1998: 98US-0079029.
XX
XX (GETH ) GENENTECH INC.
XX
XX Adams CW, Ashkenazi AJ, Chuntharapal A, Kim KJ;
XX
XX MPI: 2003-198287/19.
XX
XX N-PSDB; ABX16408.
XX
XX New Apo-2 polypeptides and polynucleotides, useful for inducing
XX apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
XX quantitative diagnostic assays, or in generating antibodies against
XX Apo-2 -
XX
XX Example 14; Fig 16; 64pp; English.
XX
XX The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
XX polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
XX or ex vivo gene therapy, in quantitative diagnostic assays, as a control
XX against samples containing unknown quantities of Apo-2, in generating
XX antibodies, in affinity purification techniques, and in competitive-type
XX receptor binding assays when labelled with, for instance, radiolodine,
XX enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
XX diagnostic for tissue-specific typing. This is the amino acid sequence
XX of the single chain antibody fragment (scFv) 20E6 used in the
XX preparation of anti-apo-2 antibodies.
XX
XX Sequence 312 AA:
XX
XX Query Match 75.2%; Score 1231; DB 24; Length 312;
XX Best Local Similarity 77.7%; Pred. No. 1.2e-75;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4:
XX
XX 1 MTMTPTSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVDSGGGVOPGRLRLS 60
XX 1 MTMTPTSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVDSGGGVOPGRLRLS 60
XX
XX 61 CAASGTFSSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX 61 CAASGTFSSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX
XX 121 QMNSLRAEDTAVYYCARD-----RgyyMDVMGKTTVYSSGGSGSGGSGGGS 172
XX 121 QMNSLRAEDTAVYYCARD-----RgyyMDVMGKTTVYSSGGSGSGGSGGGS 172
XX
XX 173 QSVLTQPPSVSGAPGQRTVISTGTRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSCV 232
XX 173 -SELTDQPAVSVALGQTVRITCOGDSLR---SYIASWYQOKPGQAPVLYIYKKNRPSGI 234
XX
XX 233 PRFGSGRSGTASLAITGLQAEDEADYVCOYSDSLRSGVPGGKRYVTLGAHHHHH 292
XX 233 PRFGSSSSGNTASLITITGAQAEDEADYVCOYSDSLRSGVPGGKRYVTLGAHHHHH 294
XX
XX 293 HGAAEOKLISEDLNGAA 310
XX 295 HGAAEOKLISEDLNGAA 312
XX
XX Db

```

[illegible]

Db	61	ADSVKGRFTTISHDNSKNLTLYQMNLSRAEDTAIVYCAKROYDILITGYGGFDYWGQCTWV	120
Oy	154	TVSSGGGGGGGGGGGGGGS-QSVLRDPSPVSGAPGORYISCTGRSSNIGAGHDVHWYQO	212
Db	121	TVSSGGGGGGGGGGGGGGAQAVLRDPSPVSGAPGORYISCTGRSSNIGAGHDVHWYQO	180
Oy	213	LPGTAPKLLIYDSDNRPSCVDPDRFGSGRSRGTSAISLAITGLQADEADYVYCOQSDSLRGS	272
Db	181	PFGTAPKLLIYGNNNRPSGVDPDRFSVSKSGTSASLAITGLQADEADYVYCOQSDSLSGT	240
Oy	273	VFGGKTATVLCG	284
Db	241	IFGTGKTATVLCG	252
RESULT 11			
ABP44977	ID	ABP44977 standard; Protein; 252 AA.	
XX	AC	ABP44977;	
XX	DT	19-AUG-2002 (first entry)	
XX	DE	Human Blys binding scFv SEQ ID 988.	
XX	XX	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;	
XX	XX	tumour necrosis factor; B cell proliferation; B cell differentiation;	
XX	XX	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;	
XX	XX	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;	
XX	XX	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	
XX	XX	common variable immunodeficiency; acquired immunodeficiency syndrome.	
OS		Homo sapiens.	
PN		WO200202641-A1.	
XX	PD	10-JAN-2002.	
XX	PD	15-JUN-2001; 2001WO-US19110.	
XX	PF	16-JUN-2000; 2000US-212210P.	
PR	PR	17-OCT-2000; 2000US-240816P.	
PR	PR	16-MAR-2001; 2001US-276248P.	
PR	PR	21-MAR-2001; 2001US-277379P.	
PR	PR	25-MAY-2001; 2001US-293499P.	
XX	PA	(HUKA-) HUMAN GENOME SCT INC.	
XX	PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
XX	PI	Ruben SM, Barash SC, Chol GH, Vaughan T, Hilbert D;	
XX	XX	WPI; 2002-114799/15.	
DR			
PT		Antibodies against B Lymphocyte Stimulating polypeptides, useful for	
PT		the diagnosis and treatment of cancers and immune disorders -	
XX			
XX			
PS		Claim 1; Page 1580-1581; 3148pp; English.	
CC		This invention describes novel antibodies that immunospecifically bind to	
CC		B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the	
CC		tumour necrosis factor (TNF) super family and induces B cell	
CC		proliferation and differentiation. The antibodies of the invention have	
CC		cytostatic, immunosuppressive, immunostimulant, immunomodulatory,	
CC		antirheumatic and antiAIDS activity and can be used in vaccines to	
CC		inhibit the expression and activity of Blys. The antibodies bind to Blys	
CC		and so may be used to detect and quantitate the presence of Blys in	
CC		biological samples and may be used in this way to diagnose disease	
CC		associated with aberrant expression of Blys. They may also be	
CC		administered to treat diseases associated with aberrant Blys expression	
CC		and activity such as cancer, immune, and autoimmune disorders and	
CC		diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,	
CC		immunodeficiency (e.g. common variable immunodeficiency (CVID) and	
CC		acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent	

CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.

SQ Sequence 252 AA;

Query Match 66.5%; Score 1089.5; DB 23; Length 252;

Best Local Similarity 83.4%; Pred. No. 37e-66;

Matches 211; Conservative 14; Mismatches 19; Indels 9; Gaps 3;

40 QVLTQVSGGGVQVQPSRLRLSCAASGFTFSSYGMHWQAPQKGLWVAGIFYDGKNTY 99

1 EVQLVESGGGVQVQPSRLRLSCAASGFTFSSYGMHWQAPQKGLWVALLIYDSKITY 60

100 ADVKGRFTISRDNKNTLYLQMSLRADRAVYVCARDR-----GYMDWVGKGT 152

61 ADVKGRFTISRDNKNTLYLQMSLRADRAVYVCARSHYDILGLTWYFDLWGRGL 120

153 TVTSSGGGGGGGGGGSSQSVLTQPPSVSAPQQRVTISCTGRSSNIGAGHDVHWYQ 212

121 TVTSSGGGGGGGGGGSSQSVLTQPPSVSAPQQRVTISCTGRSSNIGAGHDVHWYQ 179

213 LPGTAPKLLIYDDSNRPSGVPDRFSGSRGTSASLAIITGLQADEADYCCSYDSLRGS 272

180 HPGKAPKLMITDYSKRPSGVPDRFSGSRGTSASLAIITGVQADEADYCCSYDSLRGS 239

273 -VFGGGRVTYVLG 284

240 RVFGTGTQYTVLG 252

RESULT 12

ID ABP45190 standard; Protein: 252 AA.

AC ABP45190;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1201.

XX Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PE 15-JUN-2001; 2001WO-US19110.

PF 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI: 2002-114799/15.

XX Antidies against B Lymphocyte Stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

XX Claim 1, Page 1835-1836, 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.

SQ Sequence 252 AA;

Query Match 66.4%; Score 1087.5; DB 23; Length 252;

Best Local Similarity 84.1%; Pred. No. 5e-66;

Matches 211; Conservative 14; Mismatches 19; Indels 7; Gaps 3;

40 QVLTQVSGGGVQVQPSRLRLSCAASGFTFSSYGMHWQAPQKGLWVAGIFYDGKNTY 99

1 EVQLVESGGGVQVQPSRLRLSCAASGFTFSSYGMHWQAPQKGLWVALLIYDSKNTY 60

100 ADVKGRFTISRDNKNTLYLQMSLRADRAVYVCARDR-----GYMDWVGKGT 153

61 ADVKGRFTISRDNKNTLYLQMSLRADRAVYVCARQYDILGLTWYFDLWGRGL 120

154 TVTSSGGGGGGGGGGSSQSVLTQPPSVSAPQQRVTISCTGRSSNIGAGHDVHWYQ 212

121 TVTSSGGGGGGGGGGSSQSVLTQPPSVSAPQQRVTISCTGRSSNIGAGHDVHWYQ 180

213 LPGTAPKLLIYDDSNRPSGVPDRFSGSRGTSASLAIITGLQADEADYCCSYDSLRGS 272

181 HPGKAPKLMITDYSKRPSGVPDRFSGSRGTSASLAIITGVQADEADYCCSYDSLRGS 240

273 -VFGGGRVTYVLG 283

241 RVFGTGTQYTVLG 251

RESULT 13

ID AAY58235 standard; Protein: 246 AA.

AC AAY58235;

DT 27-MAR-2000 (first entry)

DE Internalising anti-c-erbB-2 receptor antibody scFv F5.

XX Antibody: c-erbB-2 receptor; marker; cancer; drug targeting;

XX HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.

XX Synthetic.

OS Homo sapiens.

XX Key

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

Location/Qualifiers  
31..35  
/note= "Heavy chain variable region (VH) complementarity  
determining region 1 (CDR1)"

50..66  
/note= "VH-CDR2"

99..108  
/note= "VH-CDR3"

157..170  
/note= "Light chain variable region (VL) complementarity  
determining region 1 (CDR1)"

186..192



[illegible]

QY	219	KLIIYDDSNRPGVDRFSGSRGSSASLAITGLQAEADPADYICOSTDSLSKGVGGGT	278
Db	181	KLIIYNNRNRPGVDRFSGSRGSSASLAITGLQAEADPADYICOFYDSSLSGWFVGGGT	240
QY	279	KVTVLG 284	
Db	241	KLTVLG 246	
RESULT 14			
ABP45958			
ABP45958 standard; Protein; 243 AA.			
AC	ABP45958;		
DT	19-AUG-2002 (first entry)		
DE	Human Blys binding scFv SEQ ID 1969.		
XX			
KM	Blys: B lymphocyte stimulator; TNF superfamily; human; cytosolic;		
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;		
KM	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;		
KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;		
KM	systemic lupus erythematosus; Rheumatoid arthritis; CYID; AIDS;		
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.		
OS	Homo sapiens.		
XX			
PN	WO200202641-A1.		
PD	10-JAN-2002.		
XX			
PF	15-JUN-2001; 2001WO-US19110.		
XX			
PR	16-JUN-2000; 2000US-212210P.		
PR	17-OCT-2000; 2000US-240816P.		
PR	16-MAR-2001; 2001US-276248P.		
PR	21-MAR-2001; 2001US-277379P.		
XX	25-MAY-2001; 2001US-293499P.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hlibert D;		
DR	WPI: 2002-114799/15.		
PS	Claim 1; Page 2750-2751; 3148pp; English.		
CC	This invention describes novel antibodies that immunospecifically bind to		
CC	B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the		
CC	tumour necrosis factor (TNF) super family and induces B cell		
CC	proliferation and differentiation. The antibodies of the invention have		
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,		
CC	antirheumatic and antiAIDS activity and can be used in vaccines to		
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys		
CC	and so may be used to detect and quantitate the presence of Blys in		
CC	biological samples and may be used in this way to diagnose disease		
CC	associated with aberrant expression of Blys. They may also be		
CC	administered to treat diseases associated with aberrant Blys expression		
CC	and activity such as cancer, immune, and autoimmune disorders and		
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,		
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and		
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent		
CC	the antibodies and fragments of the antibodies described in the method		
XX	of the invention.		
SO	Sequence 243 AA;		

65.4%; Score 1071; DB 23; Length 243;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 18.3136 Seconds  
(without alignments)  
716.207 Million cell updates/sec

Title: US-10-052-798-11  
Perfect score: 1638  
Sequence: 1 MTMTIPSGAFLEIFNVK.....HHGADEQKISEDLNGAA 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents-AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1638	100.0	310	4	US-09-079-029-11 Sequence 11, Appl
2	1231.5	75.2	309	4	US-09-079-029-9 Sequence 9, Appl
3	1231	75.2	312	4	US-09-079-029-10 Sequence 10, Appl
4	989.5	60.4	334	4	US-09-646-028-53 Sequence 53, Appl
5	989.5	60.4	339	4	US-09-646-028-55 Sequence 55, Appl
6	983.5	60.0	348	4	US-09-646-028-51 Sequence 51, Appl
7	924.5	56.4	280	3	US-09-184-658-40 Sequence 40, Appl
8	908.5	55.5	284	3	US-09-260-527-1 Sequence 1, Appl
9	905	55.3	249	4	US-10-039-785-53 Sequence 53, Appl
10	877	53.5	245	4	US-08-918-148-76 Sequence 76, Appl
11	849	51.8	258	2	US-08-665-202-5 Sequence 5, Appl
12	849	51.8	258	4	US-09-315-574-5 Sequence 5, Appl
13	848.5	51.8	297	4	US-09-486-814A-2 Sequence 2, Appl
14	839	51.2	255	4	US-09-553-498-8 Sequence 8, Appl
15	839	51.2	255	4	US-09-618-869-8 Sequence 8, Appl
16	833.5	50.9	301	2	US-08-661-052-14 Sequence 14, Appl
17	833.5	50.9	301	3	US-09-188-082-14 Sequence 14, Appl
18	833.5	50.9	301	4	US-09-364-088-14 Sequence 14, Appl
19	833.5	50.9	301	4	US-09-102-716-14 Sequence 14, Appl
20	827.5	50.5	284	3	US-08-564-164A-2 Sequence 2, Appl
21	825	50.4	244	4	US-08-918-148-78 Sequence 78, Appl
22	821.5	50.2	244	4	US-08-918-148-79 Sequence 79, Appl
23	821	50.1	289	3	US-09-184-658-63 Sequence 63, Appl
24	819.5	50.0	244	4	US-08-918-148-77 Sequence 77, Appl
25	811	49.5	245	4	US-08-918-148-75 Sequence 75, Appl
26	803.5	49.1	244	4	US-10-039-785-44 Sequence 44, Appl
27	800.5	48.9	278	3	US-09-260-527-3 Sequence 3, Appl

28	797	48.7	281	4	US-09-025-769B-178 Sequence 178, App
29	791	48.3	282	2	US-08-860-174A-10 Sequence 10, Appl
30	790.5	48.3	250	4	US-10-039-785-50 Sequence 50, Appl
31	788	48.1	245	4	US-10-039-785-42 Sequence 42, Appl
32	788	48.1	245	4	US-10-039-785-46 Sequence 46, Appl
33	785	47.9	249	4	US-08-918-148-74 Sequence 74, Appl
34	779.5	47.6	236	2	US-08-190-199A-65 Sequence 65, Appl
35	779.5	47.6	553	3	US-08-661-052-16 Sequence 16, Appl
36	779.5	47.6	553	3	US-09-188-082-16 Sequence 16, Appl
37	779.5	47.6	553	4	US-09-364-088-16 Sequence 16, Appl
38	779.5	47.6	553	4	US-09-102-716-16 Sequence 16, Appl
39	777	47.4	245	4	US-10-039-785-43 Sequence 43, Appl
40	774	47.3	245	4	US-10-039-785-48 Sequence 48, Appl
41	772	47.1	245	4	US-10-039-785-49 Sequence 49, Appl
42	769.5	47.0	240	2	US-08-956-047-25 Sequence 25, Appl
43	766	46.8	245	4	US-10-039-785-45 Sequence 45, Appl
44	764.5	46.7	267	4	US-09-485-737B-2 Sequence 2, Appl
45	760.5	46.4	277	2	US-08-256-790-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-079-029-11  
Sequence 11, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuncharapal, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079, 029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maerschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-11  
Query Match 100.0%; Score 1638; DB 4; Length 310;  
Best Local Similarity 100.0%; Pred. No. 5.2e-120;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTMTIPSGAFLEIFNVKLLFAIPLYVPPFAQAQAQVQVQSGGQVQPGKSLLS 60  
DB 1 MTMTIPSGAFLEIFNVKLLFAIPLYVPPFAQAQAQVQVQSGGQVQPGKSLLS 60  
QY 61 CAASGFIRSYSGMHVVRQAPGKLEWVAGIFYDGNKTYVDSVKGRFTISRDNKNTLYL 120

```
Db 61 CAASGTFSSYGMHWROAPGKLEWVAGIFDYGNKMYADSVKGRFTISRDNKNTLYL 120
QY 121 QNMSLAEDTAVYYCAR-----DRGYTMDVWGKTTVTVSSGGGSGGGGSGGGSQSVL 176
Db 121 QNMSLAEDTAVYYCAKILGAGRWYF-DLMGKTTVTVSSGGGSGGGGSGGGS-SEL 178
QY 121 QNMSLAEDTAVYYCARDKRYTMDVWGKTTVTVSSGGGSGGGGSGGGSQSVLTQPP 180
Db 121 QNMSLAEDTAVYYCARDKRYTMDVWGKTTVTVSSGGGSGGGGSGGGSQSVLTQPP 180
QY 181 SVSAGPQRYTISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSDNRPSGVPDRFSGSR 240
Db 181 SVSAGPQRYTISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSDNRPSGVPDRFSGSR 240
QY 241 SGTSAELATITGLQAEDEADYVCSYDSSLRGSVFGGGRKVTYVLAAGAAHHHHHGAAGQKL 300
Db 241 SGTSAELATITGLQAEDEADYVCSYDSSLRGSVFGGGRKVTYVLAAGAAHHHHHGAAGQKL 300
QY 301 ISEEDINGAA 310
Db 301 ISEEDINGAA 310
```

## RESULT 2

```
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9
```

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Query Match 75.2%; Score 1231.5; DB 4; Length 309;
Best Local Similarity 78.0%; Pred. No. 2.1e-88;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;
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QY 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAOVLVOSGGVGPGRSLRLS 60
Db 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAEVDLVOSGGVERGSLRLS 60
QY 61 CAASGTFSSYGMHWROAPGKLEWVAGIFDYGNKRYADSVKGRFTISRDNKNTLYL 120
Db 61 CAASGTFPDYGMHWROAPGKLEWVAGISINNNGSGTADSVKGRFTISRDNKNTLYL 120
```

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QY 121 QNMSLAEDTAVYYCAR----DRGYTMDVWGKTTVTVSSGGGSGGGGSGGGSQSVL 176
Db 121 QNMSLAEDTAVYYCAKILGAGRWYF-DLMGKTTVTVSSGGGSGGGGSGGGS-SEL 178
QY 177 TOPPSVAGPQRYTISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSDNRPSGVPDRF 236
Db 177 TOPPSVAGPQRYTISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSDNRPSGVPDRF 236
QY 237 SGTSAELATITGLQAEDEADYVCSYDSSLRGSVFGGGRKVTYVLAAGAAHHHHHGAAG 296
Db 236 SGTSAELATITGLQAEDEADYVCSYDSSLRGSVFGGGRKVTYVLAAGAAHHHHHGAAG 296
QY 297 EOKLISEEDINGAA 310
Db 296 EOKLISEEDINGAA 309
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## RESULT 3

```
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10
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Query Match 75.2%; Score 1231; DB 4; Length 312;
Best Local Similarity 77.7%; Pred. No. 2.4e-88;
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
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QY 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAOVLVOSGGVGPGRSLRLS 60
Db 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAGVQLVSGGGLVPGGSLRLS 60
QY 61 CAASGTFSSYGMHWROAPGKLEWVAGIFDYGNKRYADSVKGRFTISRDNKNTLYL 120
Db 61 CAASGTFSSYGMHWROAPGKLEWVAGIFDYGNKRYADSVKGRFTISRDNKNTLYL 120
QY 121 QNMSLAEDTAVYYCARD-----RGYYTMDVWGKTTVTVSSGGGSGGGGSGGGS 172
Db 121 QNMSLAEDTAVYYCARDLLKYGSSSGWF--DPMGRGTTVTVSSGGGSGGGGSGGGS 178
```

```

QY 173 OSVLTQPPSYGARGVHTTSCGRSSNIGAGHDVHYQQLPCTAPKLLIYDSDNRPSGV 232
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 -SELTQPPASVALGQVVRITCGDSLRL---SYASWYQKPGAPVLVIYIGKNNRSGI 234
QY 233 PDRSGSRGTSASLATGLQADEADYCOQSDSSIRGVSFGGCTVTVLGAAGHHHHH 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 PDRSGSSSGNTASLATITGAQADEADYCNRSRDSGNHVFVGCTKLTVLGAAGHHHHH 294
QY 293 HGAAGKLTSEEDNGAA 310
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 HGAAGKLTSEEDNGAA 312

```

```

RESULT 4
US-09-646-028-53
; Sequence 53, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-53

```

```

Query Match 60.4%; Score 989.5; DB 4; Length 334;
Best Local Similarity 72.5%; Pred. No. 1.6e-69;
Matches 192; Conservative 25; Mismatches 41; Indels 7; Gaps 4;

QY 33 AAOAPMAQVOLVOSGGGVOPGRSLRLSCAASGFIFSSYGMHWROAPGKLEWVAGIFY 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 AQAAPKSLVOLLSEGGGLVOSGSLRLSCVASGLTFSSALITWROAPGKLEWVAGISGF 132
QY 93 DGAHKYIADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR-GYYMDVWGKGT 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 SGDTTYADSVKGRFSSASRDNSKNTLYLQMNLRPNDAVYFCANNQGTCLDNWGQGT 192
QY 152 TVTVSS--GGGGGGGGGGGG--GQSQSVLTQPPSYGARGVHTTSCGRSSNIGAGHDVH 208
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 LVTYSSRGGGGGGGGGGGGGQSQSVLTQPPSYAARGQVHTTSCGRSSNIGAGDVN 252
QY 209 WYQQLPCTAPKLLIYDSDNRPSGVDRFSSGSRGTSASLATITGLQADEADYCOQSDYS 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 WYQKFPETAPKVLIIYSNNRPSGVDRFSSGSRGTSASLATITGLQDEDEGTYCOCDNDS 312
QY 269 LRGSVFGGCTKTVTLGAAGHHHHH 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 313 LSGWLFGGGCTKLTVL---RHNNHHH 334

```

```

RESULT 5
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P

```

```

; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

```

```

Query Match 60.4%; Score 989.5; DB 4; Length 339;
Best Local Similarity 72.5%; Pred. No. 1.6e-69;
Matches 192; Conservative 25; Mismatches 41; Indels 7; Gaps 4;

QY 33 AAOAPMAQVOLVOSGGGVOPGRSLRLSCAASGFIFSSYGMHWROAPGKLEWVAGIFY 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 AQAAPKSLVOLLSEGGGLVOSGSLRLSCVASGLTFSSALITWROAPGKLEWVAGISGF 137
QY 93 DGAHKYIADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR-GYYMDVWGKGT 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 138 SGDTTYADSVKGRFSSASRDNSKNTLYLQMNLRPNDAVYFCANNQGTCLDNWGQGT 197
QY 152 TVTVSS--GGGGGGGGGGGG--GQSQSVLTQPPSYGARGVHTTSCGRSSNIGAGHDVH 208
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 198 LVTYSSRGGGGGGGGGGGGGQSQSVLTQPPSYAARGQVHTTSCGRSSNIGAGDVN 257
QY 209 WYQQLPCTAPKLLIYDSDNRPSGVDRFSSGSRGTSASLATITGLQADEADYCOQSDYS 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 258 WYQKFPETAPKVLIIYSNNRPSGVDRFSSGSRGTSASLATITGLQDEDEGTYCOCDNDS 317
QY 269 LRGSVFGGCTKTVTLGAAGHHHHH 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 318 LSGWLFGGGCTKLTVL---RHNNHHH 339

```

```

RESULT 6
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

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```

Query Match 60.0%; Score 983.5; DB 4; Length 348;
Best Local Similarity 73.6%; Pred. No. 4.8e-69;
Matches 190; Conservative 25; Mismatches 36; Indels 7; Gaps 4;

QY 40 QVOLVOSGGGVOPGRSLRLSCAASGFIFSSYGMHWROAPGKLEWVAGIFYDGKMY 99
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 94 EVOLLSEGGGLVOSGSLRLSCVASGLTFSSALITWROAPGKLEWVAGISFGDTTY 153
QY 100 ADVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR-GYYMDVWGKTVTVSS- 157
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```



```

: GENERAL INFORMATION:
: APPLICANT: Salcedo et al.
: TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
: TITLE OF INVENTION: Receptors
: FILE REFERENCE: PR550
: CURRENT APPLICATION NUMBER: US/10/039,785
: CURRENT FILING DATE: 2002-05-07
: PRIOR APPLICATION NUMBER: 60/369,860
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: 60/341,237
: PRIOR FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: 60/331,310
: PRIOR FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/331,044
: PRIOR FILING DATE: 2001-11-07
: PRIOR APPLICATION NUMBER: 60/327,364
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/323,807
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 60/309,176
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 60/294,981
: PRIOR FILING DATE: 2001-06-04
: PRIOR APPLICATION NUMBER: 60/293,473
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 53
: LENGTH: 249
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: T1006F07 scfv
US-10-039-785-53

```

```

Query Match      55.3%: Score 905; DB 4; Length 249;
Best Local Similarity 71.1%: Pred. No. 4,1e-63;
Matches 180; Conservative 24; Mismatches 37; Indels 12; Gaps 5;

QY 40 QVQLVQSGGVSVPQGRSLRLSCAASGFISSYGMHWRAQPGKLEWVAGIFPDGKYY 99
DB 1 EVQLLESGGGLVPGGSLRLSCAASGFTFSYAMSVRAQPGKLEWVSAISGSGSTYY 60
QY 100 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGYY-----YYMDVWGKGT 152
DB 61 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGYY-----YYMDVWGKGT 120
QY 153 VIVSSGGSGGGSGGGSGGS-QSVLTQPPSVSGAPGQRTVITSGTRSSNIGAGHDVWYQ 211
DB 121 VIVSSGGSGGGSGGGSGGS-QSVLTQPPSVSGAPGQRTVITSGTRSSNIGAGHDVWYQ 177
QY 212 QLTGTAPKLLIYDSSNRPSPVDFRSGSRGTSASLAITGLQAEDEADYYICOSTDSSLRG 271
DB 178 QRGQGSVLYIYDNKRPSPGIPERFSGSNSGNTATLKISGTQADEADYYICLAWDS-AD 236
QY 272 SVFGGGRKTVTLG 284
DB 237 WVEGGGRKTVTLG 249

```

```

RESULT 10
US-08-918-148-76
: Sequence 76, Application US/08918148A
: Patent No. 6343220
: GENERAL INFORMATION:
: APPLICANT: Adams, Camellia
: APPLICANT: W.
: APPLICANT: Carter, Paul J.
: APPLICANT: Fendley, Brian M.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Agonist Antibodies
: FILE REFERENCE: P0979
: CURRENT APPLICATION NUMBER: US/08/918,148A

```

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: CURRENT FILING DATE: 1997-08-25
: NUMBER OF SEQ ID NOS: 79
: SEQ ID NO 76
: LENGTH: 245
: TYPE: PRT
: ORGANISM: artificial
US-08-918-148-76

Query Match      53.5%: Score 877; DB 4; Length 245;
Best Local Similarity 71.2%: Pred. No. 6,1e-61;
Matches 178; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

QY 38 MAQVQLVQSGGVSVPQGRSLRLSCAASGFISSYGMHWRAQPGKLEWVAGIFPDGK 97
DB 1 MAEQVQLVQSGGVSVPQGRSLRLSCAASGFISSYGMHWRAQPGKLEWVAGIFPDGSE 60
QY 98 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGYYMDVWGKGTYYVSS 157
DB 61 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGSGYGMVWGRTMVTYSS 120
QY 158 GGGSGGGSGGGSGGSQSVLTQPPS-VSGAPGQRTVITSGTRSSNIGAGHDVWYQQLPCT 216
DB 121 GGGSGGGSGGGSGGSDIQMTQSPSTLSASISDRVLTTC--RASE-GLYHWLAWYQKPGK 177
QY 217 APKLLIYDSSNRPSPVDFRSGSRGTSASLAITGLQAEDEADYYICOSTDSSLRGSG 276
DB 178 APKLLIYKASSLAGAPSRFSGSGGTDFTLTISLQPDPRATYYCQY--SNYPLRFGG 235
QY 277 GTKVTVLGAA 286
DB 236 GTKLEILRAA 245

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RESULT 11
US-08-665-202-5
: Sequence 5, Application US/08665202
: Patent No. 5977322
: GENERAL INFORMATION:
: APPLICANT: Marks, James D.
: APPLICANT: Schler, Robert
: TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
: TITLE OF INVENTION: Tumor Antigens
: NUMBER OF SEQUENCES: 141
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,202
: FILING DATE: 13-JUN-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,238
: FILING DATE: 14-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,250
: FILING DATE: 15-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hunter, Tom
: REGISTRATION NUMBER: 38,498
: REFERENCE/DOCKET NUMBER: 02307E-061410
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 5:

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GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: September 22, 2003, 15:16:07 : Search time 34.2965 Seconds  
(without alignments)  
1345.823 Million cell updates/sec

Title: US-10-052-798-11  
Perfect score: 1638  
Sequence: 1 MTMTTSPGCAFFLEIFNVKK.....HHGGAECOKISEDLNGAA 310

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues  
Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PC1\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	1638	100.0	310	US-10-288-917-11	Sequence 11, Appl
2	1638	100.0	310	US-10-052-798-11	Sequence 11, Appl
3	1231.5	75.2	309	US-10-288-917-9	Sequence 9, Appl
4	1231.5	75.2	309	US-10-052-798-9	Sequence 9, Appl
5	1231	75.2	312	US-10-288-917-10	Sequence 10, Appl
6	1231	75.2	312	US-10-052-798-10	Sequence 10, Appl
7	1108.5	67.7	252	US-09-880-748-1519	Sequence 1519, Ap
8	1089.5	66.5	252	US-09-880-748-988	Sequence 988, App
9	1087.5	65.4	243	US-09-880-748-1201	Sequence 1201, Ap
10	1071	65.0	248	US-09-880-748-1890	Sequence 1890, Ap
11	1064.5	64.9	247	US-09-880-748-1953	Sequence 1953, Ap
12	1063	64.3	258	US-09-880-748-1841	Sequence 1841, Ap
13	1053.5	64.1	260	US-09-880-748-1458	Sequence 1458, Ap
14	1050.5	64.0	256	US-09-880-748-839	Sequence 839, App
15	1048.5	64.0	256	US-09-880-748-839	Sequence 839, App

16	1046.5	63.9	250	US-09-880-748-1461	Sequence 1461, Ap
17	1045.5	63.8	252	US-09-880-748-1362	Sequence 1362, Ap
18	1045.5	63.8	254	US-09-880-748-981	Sequence 981, App
19	1035.5	63.2	250	US-09-880-748-1420	Sequence 1420, Ap
20	1031	62.9	251	US-09-880-748-1309	Sequence 1309, Ap
21	1030.5	62.9	252	US-09-880-748-1627	Sequence 1627, Ap
22	1027.5	62.7	254	US-09-880-748-983	Sequence 983, App
23	1027	62.7	247	US-09-880-748-2092	Sequence 2092, Ap
24	1027	62.7	251	US-09-880-748-1542	Sequence 1542, Ap
25	1026	62.6	251	US-09-880-748-1411	Sequence 1411, Ap
26	1024	62.5	253	US-09-880-748-858	Sequence 858, App
27	1023.5	62.5	254	US-09-880-748-1759	Sequence 1759, App
28	1023	62.5	251	US-09-880-748-955	Sequence 955, App
29	1021.5	62.4	254	US-09-880-748-881	Sequence 881, App
30	1021	62.3	247	US-09-880-748-1892	Sequence 1892, Ap
31	1021	62.3	247	US-09-880-748-1978	Sequence 1978, Ap
32	1020	62.3	251	US-09-880-748-1332	Sequence 1332, Ap
33	1018	62.1	249	US-09-880-748-1956	Sequence 1956, Ap
34	1016	62.0	253	US-09-880-748-1200	Sequence 1200, Ap
35	1015.5	62.0	252	US-09-880-748-956	Sequence 956, App
36	1012.5	61.8	254	US-09-880-748-1139	Sequence 1139, Ap
37	1012	61.8	251	US-09-880-748-1317	Sequence 1317, Ap
38	1010.5	61.7	240	US-09-880-748-2105	Sequence 2105, Ap
39	1008	61.5	241	US-09-880-748-2055	Sequence 2055, Ap
40	1006.5	61.4	240	US-09-880-748-1905	Sequence 1905, Ap
41	1005.5	61.4	240	US-09-880-748-2007	Sequence 2007, Ap
42	1005.5	61.4	240	US-09-880-748-2025	Sequence 2025, Ap
43	1005.5	61.4	240	US-09-880-748-2045	Sequence 2045, Ap
44	1004.5	61.3	240	US-09-880-748-2016	Sequence 2016, Ap
45	1004.5	61.3	240	US-09-880-748-2030	Sequence 2030, Ap

## ALIGNMENTS

RESULT 1  
US-10-288-917-11  
Sequence 11, Application US/10288917  
Publication No. US20030148455A1

## GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
SREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/288,917  
FILING DATE: 06-NOV. US20030148455A1-2002  
CLASSIFICATION: <unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/052798  
FILING DATE: 02-NOV-2001  
APPLICATION NUMBER: 09/079029  
FILING DATE: 14-MAY-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-FEB-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.

```

1 REGISTRATION NUMBER: 35,600
2 REFERENCE/DOCKET NUMBER: P1101R2D1C1
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: 650/225-9416
5 TELEFAX: 650/952-9881
6 INFORMATION FOR SEQ ID NO: 11:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 310 amino acids
9 TYPE: Amino Acid
10 TOPOLOGY: Linear
11 US-10-288-917-11
12 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
13
14 Query Match 100.0%; Score 1638; DB 12; Length 310;
15 Best Local Similarity 100.0%; Pred. No. 8.4e-106;
16 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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19 Db 1 MTMITPSCGAFFLEIFNNKKLLFAFLPLVVPFFYAAAPAMAOVLVDSGGGVOPGRSLRLS 60
20 QY 61 CAASGFIRSSGGMHWROAPGKGLGEMVAGIFYDGGNKYYADSVKGRFTISRDNKNTLYL 120
21 Db 61 CAASGFIRSSGGMHWROAPGKGLGEMVAGIFYDGGNKYYADSVKGRFTISRDNKNTLYL 120
22 QY 121 QMNSTLRADTAVYYCARDRGGYYMMVMWGKGTIVTVSSGGGSGGGSGGGSQSVLTQPP 180
23 Db 121 QMNSTLRADTAVYYCARDRGGYYMMVMWGKGTIVTVSSGGGSGGGSGGGSQSVLTQPP 180
24 QY 181 SVSGAPGQGVITSCGRRSSNIGAGHDVHWYQQLPGTAPKLLIYDSDNRPDSGVDPDRSGSR 240
25 Db 181 SVSGAPGQGVITSCGRRSSNIGAGHDVHWYQQLPGTAPKLLIYDSDNRPDSGVDPDRSGSR 240
26 QY 241 SGTSAIAITGLQADEADYYCQSYDSSLRGSVFSGGKTVTVLGAANHHHHHGAAEQKL 300
27 Db 241 SGTSAIAITGLQADEADYYCQSYDSSLRGSVFSGGKTVTVLGAANHHHHHGAAEQKL 300
28 QY 301 ISEEDLNGAA 310
29 Db 301 ISEEDLNGAA 310
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31 RESULT 2
32 US-10-052-798-11
33 Sequence 11, Application US/10052798
34 Publication No. US20020150985A1
35 GENERAL INFORMATION:
36 APPLICANT: Adams, Camilia W.
37 Ashkenazi, Avi J.
38 Chuntcharapal, Anan
39 Kim, Kyung J.
40 TITLE OF INVENTION: Apo-2 Receptor
41 NUMBER OF SEQUENCES: 14
42 CORRESPONDENCE ADDRESS:
43 ADDRESSEE: Genentech, Inc.
44 STREET: 1 DNA Way
45 CITY: South San Francisco
46 STATE: California
47 COUNTRY: USA
48 ZIP: 94080
49 COMPUTER READABLE FORM:
50 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
51 COMPUTER: IBM PC compatible
52 OPERATING SYSTEM: PC-DOS/MS-DOS
53 SOFTWARE: WinPatIn.(Genentech)
54 CURRENT APPLICATION DATA:
55 APPLICATION NUMBER: US/10/052,798
56 FILING DATE: 02-No. US20020150985A1-2001
57 CLASSIFICATION: <Unknown>
58 PRIOR APPLICATION DATA:
59 APPLICATION NUMBER: US/09/079,029
60 FILING DATE: <Unknown>
61 ATTORNEY/AGENT INFORMATION:

```

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1      NAME: Marschang, Diane L.
2      REGISTRATION NUMBER: 35,600
3      REFERENCE/DOCKET NUMBER: P1101R2
4      TELECOMMUNICATION INFORMATION:
5      TELEPHONE: 650/225-5416
6      TELEFAX: 650/952-9881
7      INFORMATION FOR SEQ ID NO: 11:
8      SEQUENCE CHARACTERISTICS:
9      LENGTH: 310 amino acids
10     TYPE: Amino Acid
11     TOPOLOGY: Linear
12     SEQUENCE DESCRIPTION: SEQ ID NO: 11:
13     US-10-052-798-11
14
15     Query Match          100.0%; Score 1638; DB 14; Length 310;
16     Best Local Similarity 100.0%; Pred. No. 8,4e-106;
17     Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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19     QY      1 MFMWTFSPGAFLEIETNNVKKLLFALPLVPPFAAPMAAOYOLVQSGGGVYVQGRSLRLS 60
20     Db      1 MFMWTFSPGAFLEIETNNVKKLLFALPLVPPFAAPMAAOYOLVQSGGGVYVQGRSLRLS 60
21
22     QY      61 CAASGFIFFSYGNHWVRAQAPGKGLBVGAFIYDGGNKYYADSVYGRFTISRDN SKNTLYL 120
23     Db      61 CAASGFIFFSYGNHWVRAQAPGKGLBVGAFIYDGGNKYYADSVYGRFTISRDN SKNTLYL 120
24
25     QY      121 QMNSLRAEDTAVYYCARDRGYYTMDYWKSGKTTVTVSSGGGSGGGGSGGSGQSGLTOPP 180
26     Db      121 QMNSLRAEDTAVYYCARDRGYYTMDYWKSGKTTVTVSSGGGSGGGGSGGSGQSGLTOPP 180
27
28     QY      181 SVSGARGGVNTISCGRRSSNIGAGHDVHWYQOLGETAPKLLITLDSSNRPSGVDPDRSGSR 240
29     Db      181 SVSGARGGVNTISCGRRSSNIGAGHDVHWYQOLGETAPKLLITLDSSNRPSGVDPDRSGSR 240
30
31     QY      241 SGTSSALATLTGLQAEDEADYVQSYDSSLRGSVFGGKTVTVLGAANNNHHNGAAEQKL 300
32     Db      241 SGTSSALATLTGLQAEDEADYVQSYDSSLRGSVFGGKTVTVLGAANNNHHNGAAEQKL 300
33
34     QY      301 ISEEDLNGAA 310
35     Db      301 ISEEDLNGAA 310
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37     RESULT 3
38     US-10-288-917-9
39     Sequence 9, Application US/10288917
40     Publication No. US20030148455A1
41     GENERAL INFORMATION:
42     APPLICANT: Adams, Camilla W.
43     Ashkenazi, Avi J.
44     Chuntharatpal, Anan
45     Kim, Kyung J.
46     TITLE OF INVENTION: Apo-2 Receptor
47     NUMBER OF SEQUENCES: 14
48     CORRESPONDENCE ADDRESS:
49     ADDRESSEE: Genentech, Inc.
50     STREET: 1 DNA Way
51     CITY: South San Francisco
52     STATE: California
53     COUNTRY: USA
54     ZIP: 94080
55
56     COMPUTER READABLE FORM:
57     MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
58     COMPUTER: IBM PC compatible
59     OPERATING SYSTEM: PC-DOS/MS-DOS
60     SOFTWARE: Winpatin (Genentech)
61
62     CURRENT APPLICATION DATA:
63     APPLICATION NUMBER: US/10/288,917
64     FILING DATE: 06-NO. US20030148455A1-2002
65     CLASSIFICATION: <Unknown>
66     PRIOR APPLICATION DATA:
67     APPLICATION NUMBER: 10/052798
68     FILING DATE: 02-NOV-2001
69

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APPLICATION NUMBER: 09/079029  
FILING DATE: 14-MAY-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-FEB-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-288-917-9

Query Match 75.2%; Score 1231.5; DB 12; Length 309;  
Best Local Similarity 78.0%; Pred. No. 1e-77;  
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

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DB 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60  
QY 61 CAASGFTFSYGMHVRQAPGKLEWAGIFYDGNKYYADSVKGRFTISRDNSKNTLYL 120  
DB 61 CAASGFTFDYDGMVSRQAPGKLEWAGIWMNGSGTGYADSVKGRVITISRDNAKNSLYL 120  
QY 121 QMNSLRADTAVYYCAR---DRGYIYNDVWVGKTTVYSSGGGGSGGGSGGSGQSVL 176  
DB 121 QMNSLRADTAVYYCAKILGAGRGWYF-DLWGKGTITVYSSGGGGSGGGSGGSGG-SEL 178  
QY 177 TOPPSVSGAPGQRTVISTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSDNRPSGVPDRF 236  
DB 179 TQDPVSVALGQTVKITQGDLSL--SYASWYQKQKQAPLVITIKNNRPSGIPDRF 235  
QY 237 SGRSGTASALITGLQAEDEADYYCOSYDSSLRGSVFGGKTVVLGAAHHHHHGAA 296  
DB 236 SSSSGNTASLITITGAQAEDEADYYCNSRSSGNHVVFGGKTLVLGAAHHHHHGAA 295  
QY 297 EQKLISEEDLNGAA 310  
DB 296 EQKLISEEDLNGAA 309

## RESULT 4

US-10-052-798-9  
Sequence 9, Application US/10052798  
Publication No. US20020150985A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilia W.  
Ashkenazi, Avi J.  
Chuncharapal, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/052,798  
FILING DATE: 02-No. US20020150985A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-052-798-9

Query Match 75.2%; Score 1231.5; DB 14; Length 309;  
Best Local Similarity 78.0%; Pred. No. 1e-77;  
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60  
DB 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60  
QY 61 CAASGFTFSYGMHVRQAPGKLEWAGIFYDGNKYYADSVKGRFTISRDNSKNTLYL 120  
DB 61 CAASGFTFDYDGMVSRQAPGKLEWAGIWMNGSGTGYADSVKGRVITISRDNAKNSLYL 120  
QY 121 QMNSLRADTAVYYCAR---DRGYIYNDVWVGKTTVYSSGGGGSGGGSGGSGQSVL 176  
DB 121 QMNSLRADTAVYYCAKILGAGRGWYF-DLWGKGTITVYSSGGGGSGGGSGGSGG-SEL 178  
QY 177 TOPPSVSGAPGQRTVISTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSDNRPSGVPDRF 236  
DB 179 TQDPVSVALGQTVKITQGDLSL--SYASWYQKQKQAPLVITIKNNRPSGIPDRF 235  
QY 237 SGRSGTASALITGLQAEDEADYYCOSYDSSLRGSVFGGKTVVLGAAHHHHHGAA 296  
DB 236 SSSSGNTASLITITGAQAEDEADYYCNSRSSGNHVVFGGKTLVLGAAHHHHHGAA 295  
QY 297 EQKLISEEDLNGAA 310  
DB 296 EQKLISEEDLNGAA 309

## RESULT 5

US-10-288-917-10  
Sequence 10, Application US/10288917  
Publication No. US2003014845A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilia W.  
Ashkenazi, Avi J.  
Chuncharapal, Anan  
Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/288,917  
FILING DATE: 06-NOV-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 10/052798  
FILING DATE: 02-NOV-2001  
APPLICATION NUMBER: 09/079029  
FILING DATE: 14-MAY-1998  
APPLICATION NUMBER: 60/074119  
FILING DATE: 09-FEB-1998  
APPLICATION NUMBER: 60/046615  
FILING DATE: 15-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-288-917-10

Query Match 75.2%; Score 1231; DB 12; Length 312;  
Best Local Similarity 77.7%; Pred. No. 1,1e-77;

Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFNNKKLLFAIPVPEFYAAPAMAQVQVLSGGGVPGGRSLRLS 60  
DB 1 MTMTIPSGAFLEIFNNKKLLFAIPVPEFYAAPAMAQVQVLSGGGVPGGRSLRLS 60  
QY 61 CAASGFTSSYGMHVRQAPGKGLVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
DB 61 CAASGFTSSYGMHVRQAPGKGLVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
QY 121 QNNSLRADTAVYYCARD-----RGYYMDVNGKFTYVSSGGGGSGGGSGGGGS 172  
DB 121 QNNSLRADTAVYYCARD-----RGYYMDVNGKFTYVSSGGGGSGGGSGGGGS 172  
QY 173 QSVLTQPPSVSGAPQORVYISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232  
DB 173 QSVLTQPPSVSGAPQORVYISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232  
QY 233 PDRFSGSSGTSASLITGLQAEDEADYYCOSYDSSLGSGVFGGKTATVLCGAAHHHHH 292  
DB 233 PDRFSGSSGTSASLITGLQAEDEADYYCOSYDSSLGSGVFGGKTATVLCGAAHHHHH 292  
QY 293 HGAAEQKLISEEDLNGAA 310  
DB 293 HGAAEQKLISEEDLNGAA 312

## RESULT 6

US-10-052-798-10

Sequence 10, Application US/10052798  
Publication No. US20020150985A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
Chuntharapat, Anan

TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/052,798  
FILING DATE: 02-NOV-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-052-798-10

Query Match 75.2%; Score 1231; DB 14; Length 312;  
Best Local Similarity 77.7%; Pred. No. 1,1e-77;

Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFNNKKLLFAIPVPEFYAAPAMAQVQVLSGGGVPGGRSLRLS 60  
DB 1 MTMTIPSGAFLEIFNNKKLLFAIPVPEFYAAPAMAQVQVLSGGGVPGGRSLRLS 60  
QY 61 CAASGFTSSYGMHVRQAPGKGLVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
DB 61 CAASGFTSSYGMHVRQAPGKGLVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120  
QY 121 QNNSLRADTAVYYCARD-----RGYYMDVNGKFTYVSSGGGGSGGGSGGGGS 172  
DB 121 QNNSLRADTAVYYCARD-----RGYYMDVNGKFTYVSSGGGGSGGGSGGGGS 172  
QY 173 QSVLTQPPSVSGAPQORVYISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232  
DB 173 QSVLTQPPSVSGAPQORVYISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232  
QY 233 PDRFSGSSGTSASLITGLQAEDEADYYCOSYDSSLGSGVFGGKTATVLCGAAHHHHH 292  
DB 233 PDRFSGSSGTSASLITGLQAEDEADYYCOSYDSSLGSGVFGGKTATVLCGAAHHHHH 292  
QY 293 HGAAEQKLISEEDLNGAA 310  
DB 293 HGAAEQKLISEEDLNGAA 312

## RESULT 7

US-09-880-748-1519

Sequence 1519, Application US/09880748  
Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS

FILE REFERENCE: P523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1519  
;; LENGTH: 252  
;; TYPE: prt  
;; ORGANISM: Homo sapiens  
US-09-880-748-1519

Query Match 67.7%; Score 1108.5; DB 11; Length 252;  
Best Local Similarity 85.3%; Pred. No. 2.5e-69;  
Matches 215; Conservative 13; Mismatches 17; Indels 7; Gaps 3;

QY 40 QVQLVQSGGVSVPGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWVAGIFYDGANKYY 99  
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 1 QVQLDSGGGVVQPGRSRLRLSCAASGFTFSYGMHWVQAQPGKLEWVAIVISDGNKYY 60  
QY 100 ADSVKGRTISRDNSKNTLYLQMSLRADETAVYYCAQDR-----GYI-YMDVWGKGTIV 153  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 61 ADSVKGRTISRDNSKNTLYLQMSLRADETAVYYCAKQYDILGYYGGFPYWGQGTIV 120  
QY 154 TVSSGGGGSGGGSGGGS-OSVLTQPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQ 212  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 121 TVSSGGGGSGGGSGGSAQAVLTQPPSVSGAPGQRYTISCTGRSSNIGAGYDVHWYQ 180  
QY 213 LPGTAPKLLIYDSDNRPSGVPDRFSGSRSSTASLAIITGLQAEDEADYYCQSYDSLGS 272  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 181 FPGTAPKLLIYGNMNRPSGVPDRFSGSKSTASLAIITGLQAEDEADYYCQSYDSLST 240  
QY 273 VEGGKTYTVLG 284  
:||||| :  
Db 241 IFGTGTQTVLG 252

RESULT 8  
US-09-880-748-988  
;; Sequence 988, Application US/09880748  
;; Publication No. US20030059937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 988  
;; LENGTH: 252  
;; TYPE: prt  
;; ORGANISM: Homo sapiens  
US-09-880-748-988

Query Match 66.5%; Score 1089.5; DB 11; Length 252;  
Best Local Similarity 83.4%; Pred. No. 5.2e-68;  
Matches 211; Conservative 14; Mismatches 19; Indels 9; Gaps 3;  
QY 40 QVQLVQSGGVSVPGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWVAGIFYDGANKYY 99  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :

Db 1 EVQLVESGGGVVQPGRSRLRLSCAASGFTFSYGMHWVQAQPGKLEWVALLIYDGSKKYY 60  
QY 100 ADSVKGRTISRDNSKNTLYLQMSLRADETAVYYCAQDR-----GYIYMDVWGKGT 152  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 61 ADSVKGRTISRDNSKNTLYLQMSLRADETAVYYCAASHDILTGLNWFYDLWGKGL 120  
QY 153 TVSSGGGGSGGGSGGGSOSVLTQPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQ 212  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 121 TVSSGGGGSGGGSGGGSQSVLTQPPSVSAAPGQRYTISCTGRSSNIGNYY-VSWYQ 179  
QY 213 LPGTAPKLLIYDSDNRPSGVPDRFSGSRSSTASLAIITGLQAEDEADYYCQSYDSLGS 272  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 180 HPKAPKLLIYDSDNRPSGVPDRFSGSKSTASLAIITGLQAEDEADYYCQSYDSLGS 239  
QY 273 -VEGGKTYTVLG 284  
||| :||||| :  
Db 240 RVFGTGTQTVLG 252

RESULT 9  
US-09-880-748-1201  
;; Sequence 1201, Application US/09880748  
;; Publication No. US20030059937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1201  
;; LENGTH: 252  
;; TYPE: prt  
;; ORGANISM: Homo sapiens  
US-09-880-748-1201

Query Match 66.4%; Score 1087.5; DB 11; Length 252;  
Best Local Similarity 84.1%; Pred. No. 7.1e-68;  
Matches 211; Conservative 14; Mismatches 19; Indels 7; Gaps 3;

QY 40 QVQLVQSGGVSVPGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWVAGIFYDGANKYY 99  
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 1 QVQLDSGGGVVQPGRSRLRLSCAASGFTFSYGMHWVQAQPGKLEWVAIVISDGNKYY 60  
QY 100 ADSVKGRTISRDNSKNTLYLQMSLRADETAVYYCAQDR-----GYI-YMDVWGKGTIV 153  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 61 ADSVKGRTISRDNSKNTLYLQMSLRADETAVYYCAKQYDILGYYGGFPYWGKGTIV 120  
QY 154 TVSSGGGGSGGGSGGGS-OSVLTQPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQ 212  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 121 TVSSGGGGSGGGSGGSAQAVLTQPPSVSGAPGQRYTISCTGRSSNIGAGYDVHWYQ 180  
QY 213 LPGTAPKLLIYDSDNRPSGVPDRFSGSRSSTASLAIITGLQAEDEADYYCQSYDSLGS 272  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 181 FPGTAPKLLIYGNMNRPSGVPDRFSGSKSTASLAIITGLQAEDEADYYCQSYDSLGR 240  
QY 273 VEGGKTYTVLG 283  
||||| :||||| :  
Db 241 VEGGKTYTVLG 251

RESULT 10





```
Db 121 GGGSGGGGGGGGSGSVLTQPPSVSGAPGGRVTISCTGRSSNIGAGFDVHWYLOLPGR 180
QY 218 PKLIIYDSDNRPSGVPDRFSRSGTSALITGLQADEADYYCOASDSSLRSGVEGCG 277
Db 181 PKVLITGNSNRPSPGVPDRFSRSGTSASLITGLQADEADYYCOASDSSLRRAVFSTG 240
QY 278 TKVTYVLG 284
Db 241 TKVTYVLG 247

RESULT 13
US-09-880-748-1841
; Sequence 1841, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1841
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1841

Query Match 64.3%; Score 1053.5; DB 11; Length 258;
Best Local Similarity 80.2%; Pred. No. 1.6e-65;
Matches 207; Conservative 17; Mismatches 21; Indels 13; Gaps 4;

QY 40 QVALVOSGGGVOPGRSLRLSCAASGFFISSYGMHWVQAQPKGLEWVAGIFYDGNK-- 97
Db 1 EVQLVETGGGLVKPEGSLRLSCAASGFTFSISMNVRLAPKGLEWVASIRSRGGTYI 60
QY 98 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD-----RGYYY--MDVM 147
Db 61 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDPGNDILGYYYYYGMDVM 120
QY 148 GKGTIVYVSSGGSGGGGGGGGGS-QSVLTQPPSVSGAPGGRVTISCTGRSSNIGAGHD 206
Db 121 GCGTLVTVSSGGSGGGGGGSAQAVLTQPPSSVSGAPGGRVTIPCTGSSSNIRAGYD 180
QY 207 VHWYQQLPGTAPKLIYDSDNRPSGVPDRFSRSGTSASLITGLQADEADYYCOASYD 266
Db 181 VHWYQQLPGTAPKLIYDSDNRPSGVPDRFSRSGTSASLITGLQADEADYYCOASYD 240
QY 267 SLSRGSVFGGGTKVTYVLG 284
Db 241 TNLGSMWVFGGTKLTVLG 258

RESULT 14
US-09-880-748-1458
; Sequence 1458, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
```

```
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1458
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1458

Query Match 64.1%; Score 1050.5; DB 11; Length 260;
Best Local Similarity 78.5%; Pred. No. 2.6e-65;
Matches 205; Conservative 17; Mismatches 22; Indels 17; Gaps 4;

QY 40 QVALVOSGGGVOPGRSLRLSCAASGFFISSYGMHWVQAQPKGLEWVAGIFYD-GGNKY 98
Db 1 QVALVOSGGGVOPGRSLRLSCAASGFFISYAMSVWVQAQPKGLEWVSGISGNAGSNKY 60
QY 99 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD-----RGYYY-- 143
Db 61 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDPGSEYDILTYLFGYYYYG 120
QY 144 MDVWGKGTIVYVSSGGSGGGGGGGSQSVLTQPPSVSGAPGGRVTISCTGRSSNIGA 203
Db 121 MDVWGKGTIVYVSSGGSGGGGGGGSQSVLTQPPSASGPGGRVTISCSGSSNIGS 180
QY 204 GHVHWYQQLPGTAPKLIYDSDNRPSGVPDRFSRSGTSASLITGLQADEADYYCQ 263
Db 181 NTVMWYQRLPGAARQLLIYNNDRPSGIPDRFSRSGTSASLITGLQADEADYYCA 239
QY 264 SYDSSLRGSVFGGGTKVTYVLG 284
Db 240 SWDSSLNGRVFGGTKLTVLG 260

RESULT 15
US-09-880-748-839
; Sequence 839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 839
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-839
```



GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 20.9774 Seconds  
(without alignments)  
1421.159 Million cell updates/sec

Title: US-10-052-798-11

Perfect score: 1638

Sequence: 1 MTMTTSPGAFLEIFNVKK.....HHGAPDKLISEEDLNGAA 310

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750.5	45.8	268	2	A56446
2	619	37.8	249	2	S41374
3	569	34.7	128	2	S48797
4	560	34.2	122	2	E36005
5	556	33.9	233	2	JC5322
6	555.5	33.9	123	2	S38493
7	545.5	33.3	132	2	S31603
8	544	33.2	118	2	S31116
9	541.5	33.1	121	2	S19666
10	541	33.0	121	2	S51148
11	541	33.0	140	2	S70442
12	540.5	33.0	121	2	G36005
13	539	32.9	122	2	S31117
14	537	32.8	130	2	S31601
15	533.5	32.6	119	2	F36005
16	533.5	32.6	133	2	A49028
17	531.5	32.4	111	2	S36274
18	530	32.4	114	2	S46390
19	528	32.2	114	2	S46392
20	528.5	32.1	134	2	S31679
21	520	31.7	147	2	I37780
22	519.5	31.7	113	2	S38490
23	519	31.7	139	2	S31674
24	518.5	31.7	111	2	PH1645
25	517	31.6	236	2	S25746
26	516	31.5	137	2	S31701
27	514.5	31.4	130	2	PL0098
28	511.5	31.2	135	2	S31598
29	511	31.2	114	2	S46391

30	511	31.2	120	2	S31112	Ig heavy chain - h
31	508	31.0	108	2	PH1642	Ig heavy chain V r
32	507.5	31.0	125	2	S37455	Ig mu chain - huma
33	506.5	30.9	117	2	S36259	Ig heavy chain V r
34	504.5	30.8	138	2	S31666	Ig heavy chain V r
35	504	30.8	120	2	S48798	Ig heavy chain V r
36	503.5	30.7	160	2	S05271	Ig heavy chain V r
37	503	30.7	122	1	M3H0M	Ig heavy chain pre
38	502	30.6	119	2	S31111	Ig heavy chain V-I
39	501.5	30.6	119	2	S31107	Ig heavy chain - h
40	500.5	30.6	111	2	PH1643	Ig heavy chain V r
41	499.5	30.5	115	2	S36284	Ig heavy chain V r
42	499.5	30.5	122	2	S31119	Ig heavy chain - h
43	499	30.5	133	2	S31510	Ig heavy chain - h
44	496.5	30.3	120	2	S36278	Ig heavy chain V r
45	496	30.3	151	2	A60943	Ig heavy chain pre

ALIGNMENTS

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C:Accession: A56446

R:Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity dioxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-268 <TAN>

A:Cross-references: GB:020617

C:Keywords: heterotetramer; immunoglobulin

Query Match 45.8%; Score 750.5; DB 2; Length 268;

Best Local Similarity 55.2%; Pred. No. 2.1e+43;

Matches 153; Conservative 36; Mismatches 75; Indels 13; Gaps 5;

OY	38	MAOVQVVOGSGGVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIEFDGSK	97
DB	1	MAQVKLOESGAEIVKPGASVLTCTSGFNKIDYIMHWVKRPGGLEMIKRIAPANGIT	60
OY	98	YYADVXKGRFTISRDNSKNTLYIQMNSIRAEDEVYICARDGY--YMDVWKGTTVT	154
DB	61	KYDFKFGKATIAADTSNTAVYLQSLTSDTAVYCA--SYLFRYENYWGCGTTVT	117
OY	155	VSSGGGSGGGSGGGGQSIVLTQPPSV-SCAPQQRVITSGTGRSSNIGACHDVHWVOQL	213
DB	118	VSSGGGSGGGGSDSGGSDIELTQSPALMSASLEKVMWSSCRASS---VNFITYVOOK	173
OY	214	PGTAPKLLIYDSDNRPSPGDPDRFGSGRSRTASLAITGLQAEDEADYICQSDSLRGSV	273
DB	174	SDASPKLVWYTTSHLPVPRPARFSSGSGNSYSLTISMBEEDATYICQDFTS--PFT	231
OY	274	FGGGRKVTYVLCAAAHNHHHGAADOKLISEEDLNGAA	310
DB	232	FGSGTKLEIKRSAAHNHHHGAADOKLISEEDLNGAA	268

RESULT 2

S41374  
single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C:Accession: S41374

R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv anti

A:Reference number: S41374

A:Accession: S41374  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-249 <ART>  
 A:Cross-references: EMBL:Z29480

Query Match 37.8%; Score 619; DB 2; Length 249;  
 Best Local Similarity 53.4%; Pred. No. 1.3e-34;  
 Matches 134; Conservative 31; Mismatches 80; Indels 6; Gaps 4;

QY 40 QVQLVQSGGAVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKY 99  
 DB 1 QVQLVQSGGAVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKY 60  
 QY 100 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAR--GYYV---MDVWK 149  
 DB 61 VRFQDKATITADTSNTAYLLSLTSEDTAVYYCARDDLYTSLGYWGQGSTVYSSR 120  
 QY 159 GGGSGGGSGGSGSVLTQ--PPSVGAGGQRTICTGRSSNIGAGHD--VHWYQQLPG 215  
 DB 121 GGGSGGGSGGSGSDIELTQSPSVVYIGESVYSISCRSSKSLYSDGDSYLFWFLQRP 180  
 QY 216 TAPKLIYDDSNRSGVPDRFSGRSGTSASLAITGLQAEADADYCCQSYDSSLRGSVFG 275  
 DB 181 QSPQLITRMSNLASGVPRFSGSGSTFTLRISRVEADYGVYCKQHR--YPLTFG 238  
 QY 276 GGTQVTVLGA 286  
 DB 239 AGTKLELKRA 249

## RESULT 3

S48797  
 Ig heavy chain V region (anti-Sm, VH3/DxP4/JH6) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Sep-1998 #text\_change 23-Jul-1999  
 C:Accession: S48797; S26893  
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 Submitted to the EMBL Data Library, October 1994  
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A:Reference number: S48797

A:Accession: S48797  
 A:Molecule type: mRNA  
 A:Residues: 1-128 <MAH>  
 A:Cross-references: EMBL:Z46379; NID:9587147; PIDN:CAA86512.1; PID:91340168  
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of  
 A:Reference number: S26885; MUID:93021117; PMID:1404388  
 A:Accession: S26893  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: EMBL:Z12350; NID:932922; PIDN:CAA78220.1; PID:932923  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 34.7%; Score 569; DB 2; Length 128;  
 Best Local Similarity 86.7%; Pred. No. 1.4e-31;  
 Matches 111; Conservative 3; Mismatches 4; Indels 10; Gaps 2;

QY 40 QVQLVQSGGAVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKY 99  
 DB 1 QVQLVQSGGAVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKY 60  
 QY 100 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAR--GYYV---MDVWK 149  
 DB 61 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAR--GYYV---MDVWK 149  
 QY 150 GTTVTVSS 157  
 DB 121 GTTVTVSS 128

## RESULT 4

E36005  
 Ig heavy chain V region (M72) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
 C:Accession: E36005  
 R:Schroeder Jr., H.W.; Wang, J.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
 A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge  
 A:Reference number: A36005; MUID:90349571; PMID:2117273  
 A:Accession: E36005  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-122 <SCH>  
 A:Cross-references: GB:M34030  
 C:Genetics:  
 A:Gene: GDB:IGHE, IGHDY1  
 A:Cross-references: GDB:118731; OMIM:146910  
 A:Map position: 14q32.33-14q32.33  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.2%; Score 560; DB 2; Length 122;  
 Best Local Similarity 89.3%; Pred. No. 5.5e-31;  
 Matches 109; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 40 QVQLVQSGGAVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKY 99  
 DB 1 QVQLVQSGGAVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKY 60  
 QY 100 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAR--GYYV---MDVWK 149  
 DB 61 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAR--GYYV---MDVWK 149  
 QY 156 SS 157  
 DB 121 SS 122

## RESULT 5

JC5322  
 p53 specific single-chain antibody pab421 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997  
 C:Accession: JC5322  
 R:Tannot, C.B.; Hynes, N.E.  
 Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
 A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.  
 A:Reference number: JC5322; MUID:97168950; PMID:9016757  
 A:Accession: JC5322  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <JAN>  
 A:Experimental source: hybridoma cell  
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It resto

Query Match 33.9%; Score 556; DB 2; Length 233;  
 Best Local Similarity 50.4%; Pred. No. 2e-30;  
 Matches 121; Conservative 32; Mismatches 77; Indels 10; Gaps 5;

QY 45 QGGGVQPGKSLRLSCAASGFISSYGMHWVRQAPGKLEWVAGIFYDGNNKYADSVK 104  
 DB 2 ESGAEIVRSGASVKLSCTGFNIDYVHWKRPDGLWIGRIDPENGADMTRSSG 61  
 QY 105 GRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR--GYYV---MDVWK 149  
 DB 62 VRAITADTSNTAYLLSLTSEDTAVYYC--NAG--MDVWGQGVTVTVSSGGGSGG 116  
 QY 165 GGGSGGSGSVLTQ--PPSVGAGGQRTICTGRSSNIGAGHD--VHWYQQLPGTAPKLI 222  
 DB 117 RASGGGSDIELTQSPASVLAISLQGRATISCAASVSISGYSYHMQKRGQPPRLI 176



C:Accession: S51148  
 R:de Kruijf, J.; Boel, E.; Logtenberg, T.  
 submitted to the EMBL Data Library, January 1995  
 A:Description: Selection and application of human SCRV antibody fragments from a semi-sy  
 A:Reference number: S51147  
 A:Accession: S51148  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <DEK>  
 A:Cross-references: EMBL:X83713  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:13-90/Domain: immunoglobulin homology <IMM>

Query Match 33.0%; Score 541; DB 2; Length 112;  
 Best Local Similarity 92.8%; Pred. No. 9.4e-30;  
 Matches 103; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 176 LQPPVSGAPGGRVITISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSPVPR 235  
 |||||  
 DB 2 LQPPVSGAPGGRVITISCTGRSSNIGAGDVHWYQQLPCTAPKLLIYGNRNPSGVPDR 61  
 |||||  
 QY 236 FSGSRGTSASLAIITGLQAEDEADYCCQSYDSSLRGSFVGCGTKVTVLGNA 286  
 |||||  
 DB 62 FSGSKGTSASLAIITGLQAEDEADYCCQSYDSSLRGSFVGCGTKVTVLGNA 112  
 |||||

## RESULT 11

S70442

Ig heavy chain precursor V region (nu) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000

C:Accession: S70442

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A:Title: IGM kappa/Jambda EBV human B cell clone: an early step of differentiation of fe

A:Reference number: S70442; MID:93024508; PMID:1383655

A:Accession: S70442

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-140 &lt;CUI&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 33.0%; Score 541; DB 2; Length 140;  
 Best Local Similarity 86.8%; Pred. No. 1.2e-29;  
 Matches 105; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 40 QVQLVSGGQVQPGKSLRLSCAASGIFSSYGMHWROAPGKLEWVAGIFYDGSKYY 99  
 |||||  
 DB 20 QVQLVSGGQVQPGKSLRLSCAASGIFSSYGMHWROAPGKLEWVAFIRYDGSKYY 79  
 |||||  
 QY 100 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDR--GYIYMDVWGKGTYYVS 157  
 |||||  
 DB 80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDHIVGATFYDYGQGTLYVSS 139  
 |||||  
 QY 158 G 158  
 ||  
 DB 140 G 140

## RESULT 12

G36005

Ig heavy chain V region (M74) - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998

C:Accession: G36005

R:Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A:Reference number: A36005; MID:90349571; PMID:2117273

A:Accession: G36005

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-121 <SCH>  
 A:Cross-references: GB:M34031  
 C:Genetics:  
 A:Gene: GDB:IGHG; IGHDL  
 A:Cross-references: GDB:118731; OMIM:146910  
 A:Map position: 14q32.33-14q32.33  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 33.0%; Score 540.5; DB 2; Length 121;  
 Best Local Similarity 86.8%; Pred. No. 1.1e-29;  
 Matches 105; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 40 QVQLVSGGQVQPGKSLRLSCAASGIFSSYGMHWROAPGKLEWVAGIFYDGSKYY 99  
 |||||  
 DB 1 QVQLVSGGQVQPGKSLRLSCAASGIFSSYGMHWROAPGKLEWVAIVSYDGSKYY 60  
 |||||  
 QY 100 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDR--GYIYMDVWGKGTYYVS 156  
 |||||  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDKDMGALFDYWGQGTLYVVS 120  
 |||||  
 QY 157 S 157  
 ||  
 DB 121 S 121

## RESULT 13

S31117

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C:Accession: S31117

R:Raphoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp

A:Reference number: S31104; MID:92111633; PMID:1730252

A:Accession: S31117

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-122 &lt;RAA&gt;

A:Cross-references: EMBL:X62967

A&gt;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 32.9%; Score 539; DB 2; Length 122;  
 Best Local Similarity 85.2%; Pred. No. 1.4e-29;  
 Matches 104; Conservative 5; Mismatches 9; Indels 4; Gaps 1;

QY 40 QVQLVSGGQVQPGKSLRLSCAASGIFSSYGMHWROAPGKLEWVAGIFYDGSKYY 99  
 |||||  
 DB 1 QVQLVSGGQVQPGKSLRLSCAASGIFSSYGMHWROAPGKLEWVAIVSYDGSKYY 60  
 |||||  
 QY 100 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD---GYIYMDVWGKGTYYVS 155  
 |||||  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDFFAPNMSHFDYWGQGTLYV 120  
 |||||  
 QY 156 SS 157  
 ||  
 DB 121 SS 122

## RESULT 14

S31601

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31601

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from t







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:03 ; Search time 11.6541 Seconds

(Without alignments)  
1250,910 Million cell updates/sec

Title: US-10-052-798-11

Perfect score: 1638  
Sequence: 1 MTMTPTSGAFLEIFNVKR.....HHGMAEQKLSEEDLNGAA 310

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	503	30.7	122 1 HV3G_HUMAN	P01768 homo sapien
2	484.5	29.6	121 1 HV3J_HUMAN	P01771 homo sapien
3	482	29.4	126 1 HV3K_HUMAN	P01772 homo sapien
4	470.5	28.7	119 1 HV3I_HUMAN	P01770 homo sapien
5	460	28.1	122 1 HV3H_HUMAN	P01769 homo sapien
6	449.5	27.4	130 1 LV1G_HUMAN	P06316 homo sapien
7	447	27.3	136 1 HV16_MOUSE	P01783 mus musculu
8	445	27.2	112 1 LV1H_HUMAN	P06887 homo sapien
9	442.5	27.0	111 1 LV1D_HUMAN	P01702 homo sapien
10	439	26.8	116 1 HV3F_HUMAN	P01781 homo sapien
11	431.5	26.3	115 1 HV3E_HUMAN	P01767 homo sapien
12	429	26.2	117 1 HV3C_HUMAN	P01764 homo sapien
13	427.5	26.1	111 1 LV1C_HUMAN	P01701 homo sapien
14	426.5	26.0	109 1 LV1F_HUMAN	P04208 homo sapien
15	426.5	26.0	120 1 HV3E_HUMAN	P01766 homo sapien
16	424	25.9	112 1 LV1B_HUMAN	P01700 homo sapien
17	423.5	25.9	103 1 LV1E_HUMAN	P01703 homo sapien
18	423	25.8	114 1 HV3B_HUMAN	P01763 homo sapien
19	422	25.8	120 1 HV3U_HUMAN	P01782 homo sapien
20	420	25.6	119 1 HV3M_HUMAN	P01774 homo sapien
21	419.5	25.6	119 1 HV3L_HUMAN	P01773 homo sapien
22	418	25.5	119 1 HV3N_HUMAN	P01775 homo sapien
23	415.5	25.4	111 1 LV1A_HUMAN	P01699 homo sapien
24	414.5	25.3	116 1 HV05_CARAU	P19181 carassius a
25	413.5	25.2	109 1 LV1I_HUMAN	P06888 homo sapien
26	413.5	25.2	115 1 HV3D_HUMAN	P01765 homo sapien
27	413	25.2	119 1 HV38_MOUSE	P01808 mus musculu
28	411	25.1	117 1 HV3O_HUMAN	P01776 homo sapien
29	408	24.9	122 1 HV20_MOUSE	P01789 mus musculu
30	406.5	24.8	123 1 HV18_MOUSE	P01787 mus musculu
31	406.5	24.8	123 1 HV19_MOUSE	P01788 mus musculu
32	405	24.7	122 1 HV21_MOUSE	P01790 mus musculu
33	403.5	24.6	123 1 HV24_MOUSE	P01793 mus musculu

34	402	24.5	122 1 HV3A_HUMAN	P01762 homo sapien
35	401.5	24.5	123 1 HV23_MOUSE	P01792 mus musculu
36	401.5	24.5	123 1 HV25_MOUSE	P01794 mus musculu
37	400.5	24.5	123 1 HV22_MOUSE	P01791 mus musculu
38	396	24.2	119 1 HV40_MOUSE	P01810 mus musculu
39	393	24.0	112 1 LV2K_HUMAN	P04209 homo sapien
40	392	23.9	119 1 HV37_MOUSE	P01807 mus musculu
41	390.5	23.8	111 1 LV2D_HUMAN	P01707 homo sapien
42	390.5	23.8	117 1 HV02_CANFA	P01785 canis fami
43	390.5	23.8	142 1 HV01_RAT	P01805 rattus norv
44	390	23.8	117 1 HV55_MOUSE	P18526 mus musculu
45	388	23.7	117 1 HV54_MOUSE	P18525 mus musculu

ALIGNMENTS

RESULT 1	ID	HV3G_HUMAN	STANDARD	PRT	122 AA.
AC	P01768:				
DP	21-JUL-1986 (Rel. 01, Created)				
DP	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Ig heavy chain V-II region CAM.				
OS	Homo sapiens (Human).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OK	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=81013859; PubMed=6774332;				
RA	Lehman D.W., Putnam F.W.;				
RT	"Amino acid sequence of the variable region of a human mu chain:				
RT	location of a possible JH segment."				
RL	Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).				
CC	!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A				
CC	PATIENT WITH MACROGLOBULINEMIA.				
CC	!- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR: A02051, M3HUM.				
DR	HSSP; P01772; ZFB4.				
DR	GO: GO:0005576; C:extracellular; NAS.				
DR	GO: GO:0003823; F:antigen binding activity; NAS.				
DR	GO: GO:0006955; P:immune response; NAS.				
DR	InterPro: IPR007110; Ig-like.				
DR	InterPro: IPR003006; Ig-MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; Igv; 1.				
KW	PROSITE: PS50835; IG-LIKE; 1.				
KW	Immunoglobulin V region; Pyroliidone carboxylic acid.				
FT	DOMAIN 1 112				
FT	MOO_RES 1 1				
FT	NON_TER 122				
SO	SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;				

Query Match 30.7%: Score 503; DB 1; Length 122;  
Best Local Similarity 77.0%: Pred. No. 4.4e-30;  
Matches 94; Conservative 12; Mismatches 12; Indels 4; Gaps 1;

QY	40 QVQLVQSGGVSVPGRSLRLSCAASGFFSSYGMHWROAPKGLLEWVAGIFYDGSKNTY 99
DB	1 QVELVESGGGVVZGGRSLRLSCAASGFFSYGMHWROAPKGLLEWVAIVSYGBBKY 60
QY	100 ADSYKGRFTISRDNSKNTLYIQANSLRAEDTAVYYCARDR---GYTMDVWGKGTIVY 155
DB	61 ABSYKGRFTISRDNSKNTLYIQANSLRAEDTAVYYCARDRPGLYGBYRAFNWGGTIVY 120
QY	156 SS 157
DB	121 SS 122

```
RESULT 2
HV31_HUMAN
ID HV31_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HLL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG HLL";
RT Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02054; GIHURL.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliadone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610E5DAB CRC64;

Query Match 29.6%; Score 484.5; DB 1; Length 121;
Best Local Similarity 76.0%; Pred. No. 9, 6e-29;
Matches 92; Conservative 9; Mismatches 17; Indels 3; Gaps 1;

QY 40 OVQLVOSGGVQVQPGSRSLRLSCASGFTFSSYGHWVROAPGKGLRWAGITFDGKNKY 99
DB 1 OVQLVOSGGVQVQPGSRSLRLSCASGFTFSSYGHWVROAPGKGLRWAGITFDGKNKY 60
QY 100 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCARDRGY---YMDVWGKGTYYVS 156
DB 61 GDSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCARDPDLITAFSPDYWGQGLVTVS 120
QY 157 S 157
DB 121 S 121

RESULT 3
HV3K_HUMAN
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83289131; PubMed=688494;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
```

```
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguerat M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02055; GIHURL.
DR PDB: 2EB4; 12-JUL-89.
DR PDB: 2IG2; 12-JUL-89.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyroliadone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;

Query Match 29.4%; Score 482; DB 1; Length 126;
Best Local Similarity 73.8%; Pred. No. 1, 3e-28;
Matches 93; Conservative 14; Mismatches 11; Indels 8; Gaps 1;

QY 40 OVQLVOSGGVQVQPGSRSLRLSCASGFTFSSYGHWVROAPGKGLRWAGITFDGKNKY 99
DB 1 OVQLVOSGGVQVQPGSRSLRLSCSSGFTFSSYAMTWVROAPGKGLRWAGITFDGSDQHY 60
QY 100 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCARDRGY-----DVGKGT 151
DB 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCARDGSGHFCSSASCGPDYWGQGT 120
QY 152 TVTVSS 157
DB 121 PTVVSS 126

RESULT 4
HV31_HUMAN
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ID HV31_HUMAN STANDARD: PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponsitngl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGL MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A91668; G1HUNI.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG-V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliadone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULF 22 96
FT NON_TER 119 119
SO SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;

Query Match 28.7%; Score 470.5; DB 1; Length 119;
Best Local Similarity 76.7%; Pred. No. 9.8e-28;
Matches 92; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

OY 40 QVQLVSGGAVGPGRSLRLSCAASGFTSSYGMHWQAQPGKLEWAGIFYDGKNRY 99
DB 1 QVQLVSGGAVGPGRSLRLSCAASGFTSSYGMHWQAQPGKLEWAVVSSBGBXYY 60
OY 100 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYYCA--RRGYIYMDVWGKGTIVYSS 157
DB 61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYYCA--RRGYIYMDVWGKGTIVYSS 119

RESULT 5
HV31_HUMAN STANDARD: PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins."
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02052; M3HUGA.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG-V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliadone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SO SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 28.1%; Score 460; DB 1; Length 122;
Best Local Similarity 68.9%; Pred. No. 5.8e-27;
Matches 84; Conservative 18; Mismatches 16; Indels 4; Gaps 1;

OY 40 QVQLVSGGAVGPGRSLRLSCAASGFTSSYGMHWQAQPGKLEWAGIFYDGKNRY 99
DB 1 QVQLVSGGAVGPGRSLRLSCAASGFTSSYGMHWQAQPGKLEWAVVSSBGBXYY 60
OY 100 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYYCA---RGYIYMDVWGKGTIVY 155
DB 61 AASVKGRTISRDNKNTLYIQMNSLRADPAVYYCA---RGYIYMDVWGKGTIVY 120
OY 156 SS 157
DB 121 SS 122

RESULT 6
LVIG_HUMAN STANDARD: PRT; 130 AA.
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
RT sequence."
RL Nucleic Acids Res. 12:8407-8414(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL, X01147; CAA25598.1; -.

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DR PIR: A01966; LIHUBL.
DR HSSP: P01703; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-Like.
DR InterPro: IPR003596; Ig-LV.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-Like; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BEL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON_TER 130 130
SQ SEQUENCE 130 AA: 13564 MW: FA44BBL7D3A55BDF CRC64;

Query Match 27.4%; Score 449.5; DB 1; Length 130;
Best Local Similarity 74.1%; Pred. No. 3.6e-26;
Matches 86; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 169 GGGGSSVLTQPPSVSGAPGQRTISTGSSNSINGAGHDVHWQQLFGTPAKLLIYDSSNR 228
DB 16 GSAQSVLTQPPSVSAPGQKVTISGSSNSINGNDY-VSWYQVGPATPKLLIYDNNKR 74
QY 229 PGGVPRFSGSRSGTSASLAITGLQAEADADYCYCOSYDSSLRGSVFGGKTATVLG 284
DB 75 PGGIPRFGSGSKSGTSATIGITGLQIGDADYCCGTWNSLSGWVFGGKTATVLG 130

RESULT 7
HVL6_MOUSE STANDARD: PRT: 136 AA.
ID HVL6_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Karl T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
RN [3]
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: J00522; AAD15290.1; -.
DR PIR: E90809; GIMS21.
DR PDB: 1IGC; 03-JUN-95.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.

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DR InterPro: IPR003596; Ig-LV.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-Like; 1.
KM Immunoglobulin V region; Signal: 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 J44 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT NON_TER 136 136 Y -> W (IN REF. 2).
SQ SEQUENCE 136 AA: 15071 MW: 2276A98DBDBF7016 CRC64;

Query Match 27.3%; Score 447; DB 1; Length 136;
Best Local Similarity 73.1%; Pred. No. 5.7e-26;
Matches 87; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 41 VOLVGGGVPGRSLRSCAASGFIFSSYGMHWVROAPGKLEWVAGIFYDGGNKXYA 100
DB 18 VOLVESGGELVPGGSRKLSCAASGFTSSFGEMHWROAPEKLEWVAIISGSSLTLYA 77
QY 101 DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYGCAR--DRGYVYMDYWGKGTIVVSS 157
DB 78 DTVKGRFTISRDNKNTLYLQMNSLRAEDTAVYGCAR--DRGYVYMDYWGKGTIVVSS 136

RESULT 8
LV1H_HUMAN STANDARD: PRT: 112 AA.
ID LV1H_HUMAN
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
CC WERE POSITIONED BY HOMOLOG.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC MARKERS.
CC -----
DR -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A25479; LIHDM.
DR HSSP: P01703; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-Like.
DR InterPro: IPR003596; Ig-LV.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-Like; 1.
KM Immunoglobulin V region; Monoclonal antibody;
KW Pyroglutamate carboxylic acid.
FT DOMAIN 1 106
FT MOD_RES 1 1 IG-LIKE.
FT DISULFID 22 90 PYROGLUTAMATE CARBOXYLIC ACID.
FT NON_TER 112 112 BY SIMILARITY.
SQ SEQUENCE 112 AA: 11789 MW: 748124F079CFB84 CRC64;

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Query Match      27.2%; Score 445; DB 1; Length 112;
Best Local Similarity 76.6%; Pred. No. 6.4e-26;
Matches 85; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

OY 173 QSVLTQPPSVSGAPGQRTVICTGRSSNIGAGHDVHWQQLPGTAPKLLIYDDSRPSGV 232
DB 1 QSVLTQPPSVSGAPGQRTVICTGRSSNIGAGHDVHWQQLPGTAPKLLIYNNQRPSPGV 60
OY 233 PDRESGSRGTSASLAITGLOAEDADYCCOSYDLSGVSFGGTXTVL 283
DB 61 PDRESGSRGTSASLAITGLOAEDADYCCOSYDLSGVSFGGTXTVL 111

RESULT 9
ID LV1D_HUMAN STANDARD: PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup.",
RT J. Biochem. 93:421-429(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A01965; LIHNG.
DR HSSP: P01703; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Pyroglutamate carboxylic acid.
KW DOMAIN
FT MOD_RES 1 105 PYROGLUTAMATE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match      27.0%; Score 442.5; DB 1; Length 111;
Best Local Similarity 76.8%; Pred. No. 9.6e-26;
Matches 86; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

OY 173 QSVLTQPPSVSGAPGQRTVICTGRSSNIGAGHDVHWQQLPGTAPKLLIYDDSRPSGV 232
DB 1 QSVLTQPPSVSGAPGQRTVICTGRSSNIGAGHDVHWQQLPGTAPKLLIYNNQRPSPGI 59
OY 233 PDRESGSRGTSASLAITGLOAEDADYCCOSYDLSGVSFGGTXTVL 284
DB 60 PDRESGSRGTSASLAITGLOAEDADYCCOSYDLSGVSFGGTXTVL 111

RESULT 10
ID HV3T_HUMAN STANDARD: PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H II. Architecture of the complete IgM-molecule.",
RT Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR: A02064; M3HUGL.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match      26.8%; Score 439; DB 1; Length 116;
Best Local Similarity 72.9%; Pred. No. 1.8e-25;
Matches 86; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

OY 40 QVLTQSGGQVYQPERSLRLSCASGFTFSYGMHWQAPGKLEWVAGIFYDGCKRY 99
DB 1 EVQLTSGGQVYQPERSLRLSCASGFTFSYGMHWQAPGKLEWVAGIFYDGCKRY 60
OY 100 ADVYKGRFTISDNKNTLYLQMSLRVEDTAVYCCADRGYYVDWVGKTTVYSS 157
DB 61 VDSYKGRFTISDNKNTLYLQMSLRVEDTAVYCCADRGYYVDWVGKTTVYSS 116

RESULT 11
ID HV3F_HUMAN STANDARD: PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT 19A2 immunoglobulin of the A2m (2) allotype.",
RT Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; A2H0BU.
DR HSSP: P01789; 1MCP.

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DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS0835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 111
FT NON_TER 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCE4 CRC64;

Query Match
Best Local Similarity 71.2%; Pred. No. 6.3e-25;
Matches 84; Conservative 15; Mismatches 16; Indels 3; Gaps 2;

QY 40 QVQLVQSGGVSVPQGRSLRLSCAASGFTFSYGMHWVQAPGKGLEWVAGIFYDGANKYY 99
DB 1 EVQLVETGGGLIQPGSLRLSCAASGFTVSBHSMVVRQAPGKALZWVSAI-YRGGTTY 59

QY 100 ADSVAGRTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGYNDYMGKGTYYSS 157
DB 60 ADSVAGRTISRDNSHRYVYLOMBSLRAEDTAVYYCARDLA--AARLFEGKGTYYSS 115

RESULT 12
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Mathysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC
DR EMBL: J00236; AAA53516.1; -
DR EMBL: M35415; AAA58735.1; -
DR PIR: A02047; H3H026.
DR PDB: 1HOU; 23-DEC-99.
DR Genew; HGNC:5545; IGHV6.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS0835; IG-LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-II REGION VH26.

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FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match
Best Local Similarity 82.7%; Pred. No. 9.7e-25;
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 40 QVQLVQSGGVSVPQGRSLRLSCAASGFTFSYGMHWVQAPGKGLEWVAGIFYDGANKYY 99
DB 20 EVQLLESQGLVQPGSLRLSCAASGFTFSYAMSVVRQAPGKLEWVSAISGSGSTYY 79

QY 100 ADSVAGRTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 137
DB 80 GDSVAGRTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117

RESULT 13
LV1C_HUMAN
ID LV1C_HUMAN STANDARD; PRT; 111 AA.
AC P01701;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Ig lambda chain V-I region NEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69060892; PubMed=4177823;
RA Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein New (lambda-
RT type). Subgroups in the variable part of immunoglobulin L-chains of
RT the lambda-type."; Physiol. Chem. 349:945-951(1968).
RL Hoppe-Seyler's Z. Physiol. Chem.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A01964; LIH0NW.
DR HSSP: P01703; 7FAB.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS0835; IG-LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein;
KW Pyroglutamate carboxylic acid.
FT DOMAIN 1 105
FT MOD_RES 1 1 PYROGLUTAMINE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11453 MW; AABCBCA3C49F2AD3 CRC64;

Query Match
Best Local Similarity 73.2%; Pred. No. 1.2e-24;
Matches 82; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 173 QSVLTQPPSPVSGAPQGRVYISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV 232
DB 1 GSVLTPPSPVSAAPQGRVYISCTSGSGSTNGNNY-VSMHQHLPGTAPKLLIYEDNKRPSGI 59

QY 233 PDRFSGSRGTSASLAITGLQAEADADYICQSYDSSLRKSVAGGKTYVLG 284
DB 60 PDRISAKSGTSATITGLRTGDEADYVCAWDSLLNAVVFVGKTYVLG 111

RESULT 14
LV1F_HUMAN

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ID LV1F\_HUMAN STANDARD: PRT: 109 AA.  
AC P04208;  
DR 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-I region WAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83221661; PubMed=6407018;  
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;  
RT "Complete covalent structure of a human immunoglobulin D: sequence of  
RT the lambda light chain";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).  
DR PIR: A01967; LIHWA.  
DR HSSP: P01703; 7FAB.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig-MHC.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 97 V SEGMENT.  
FT DOMAIN 98 109 J SEGMENT.  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA: 11725 MW: 817785F6A8DF9BAC CRC64;

Query Match 26.0%; Score 426.5; DB 1; Length 109;  
Best Local Similarity 76.6%; Pred. No. 1.4e-24;  
Matches 85; Conservative 10; Mismatches 13; Indels 3; Gaps 2;

OY 173 QSVLTQPPSVGARGQRTICTGRSSNIGAGHDYHWYQQLPGTAPKLLIYDDSNRPSGV 232  
DB 1 QSVLTQPPSVGARGQRTICTGRSSNIGAGHDYHWYQQLPGTAPKLLIYDDSNRPSGV 59  
OY 233 PDRESGSRGTASALATGLOAEDADYCCSYDSSLRGVFGGTXTVL 283  
DB 60 PDRESGSRGTASALATGLOAEDADYCCSYDSSLRGVFGGTXTVL 108

## RESULT 15

HV3E\_HUMAN STANDARD: PRT: 120 AA.  
AC P01766;  
DR 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region BRO.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77117674; PubMed=65324;  
RA Capra J.D., Hopper J.E.;  
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an  
RT individual patient. III. The complete amino acid sequence of the VH  
RT region of the IgM paraprotein.";  
RL Immunohistochemistry 13:995-999(1976).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE  
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM  
CC TYPE.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC PIR: A02049; M3HUBW.

DR HSSP: P01772; 2FBA.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig-MHC.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 111 IG-LIKE.  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA: 13227 MW: D3F0428F7C2E6410 CRC64;

Query Match 26.0%; Score 426.5; DB 1; Length 120;  
Best Local Similarity 70.8%; Pred. No. 1.5e-24;  
Matches 85; Conservative 10; Mismatches 16; Indels 9; Gaps 2;

OY 40 QVLTQSGGAGVYQPGSRSLRLSCAASGFTFSSYGMHWQAPGKGLDWMVAGIFYDGKRY 99  
DB 1 EVLTQSGGAGVYQPGSRSLRLSCAASGFTFSSYGMHWQAPGKGLDWMVAGIFYDGKRY 59  
OY 100 ADSVKGRTTISRDNKNTLYLQMSLRADTAAYVYCARD-----RQYYMDYWGKGT 151  
DB 60 ADSVKGRTTISRDNKNTLYLQMSLRADTAAYVYCARDSPVSLVDGWLTYYYGVSVMGQGT 119

Search completed: September 22, 2003, 15:13:49  
Job time : 12.6541 secs







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QY 61 CAASGTFSSYGMHWVROAPGKLEWVAGIFPDGKNKYADSVKGRFTISRDNKNTLYL 120
DB 61 CAASGDSFGRWMSWVROAPGKLEWIGEIFNPDSSITNTYPSLKDFIISRDNKNTLYL 120
QY 121 OMNSLRAPEDTAYVYCGARDGYVMDVWGCTVTYVSSGGSGSGSGSGSVLTQ-P 179
DB 121 QMSKVSSEDTALYCARASYGHSAYWGGCTVTYVSSGGSGSGSGSDIELTQSP 180
QY 180 PVSAGAPGQRTVTSCTGRSSNIGAGHD-VHWYQQLTGTPAKLTIYDSSNRPSGVPDRFSG 238
DB 181 ASLASVGETVTITCCA-SGNT--HNLYAWQOKGKSPQLLYVAKTLADGVPFRFSG 236
QY 239 SSGSTASALATITGLAEDADYVYCGSYDSSLRGSGVFGGCTKYTVIGAAA 287
DB 237 SSGSTQYSIKINSLOPEDEFGSYCQHFMTT--PYTGGGKLEIKRAAA 283

RESULT 2
Q921A6 PRELIMINARY: PRT: 241 AA.
AC Q921A6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ancl-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98170165; PubMed-9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Shih P.G., Ryu S.H., Chung H.K.;
RT Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL: U88067; AAB48044.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IgV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1
FT TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248BE9C771 CRC64;

Query Match 37.0%; Score 606.5; DB 11; Length 241;
Best Local Similarity 50.8%; Pred. No. 6.1e-38;
Matches 127; Conservative 33; Mismatches 67; Indels 23; Gaps 6;

QY 40 QYQVLVSGGGVQPGSLRLSCAASGFTIRSSYGMHWVROAPGKLEWVAGIFPDGKNKY 99
DB 1 QYKVLQOSGELKRPGETVVKISCAKASYPTDYGMNVKQAPGKLMWGMINTYDEPY 60
QY 100 ADVSKGRFTISRDNKNTLYLQMSLRAPEDTAVVYCARGRVYVMDVWGCTVTYVSSG 159
DB 61 ADDFKRFAFSLSTASTAYLQINNKNDIATYFARADLRYFYWQGGITVYVSSG 120
QY 160 GSGSGSGSGGGSQSVLTQ-PVSAGAPGQRTVTSCTGRSSNIGAGHDVH---WYQQLP 214
DB 121 GSGSGSGSGGSDIELTQSPSLASLGKVTITCK-----ASQDINKYIAWYQHNP 173
QY 215 GRAPK---LTIYDSSNRPSGVPDRFSGSGTSASLAITGLAEDADYVYCGSYDSSLR 270
DB 174 GKGPRASARTIHTIYIQ---PGIPSRPSGSGSDYFSFISNLEPEDIAIYATYCIHYDNL-- 227
QY 271 GSVFGGGTRKY 280
DB 228 -HTFGGGTKL 236

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RESULT 3
Q8WUK1 PRELIMINARY: PRT: 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=tonsil;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020240; AAB20240.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_5.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F9590671E315 CRC64;

Query Match 33.3%; Score 546; DB 4; Length 613;
Best Local Similarity 84.0%; Pred. No. 6.7e-33;
Matches 105; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

QY 40 QYQVLVSGGGVQPGSLRLSCAASGFTIRSSYGMHWVROAPGKLEWVAGIFPDGKNKY 99
DB 20 QYQVLVSGGGVQPGSLRLSCAASGFTIRSSYGMHWVROAPGKLEWVAGIFPDGKNKY 79
QY 100 ADVSKGRFTISRDNKNTLYLQMSLRAPEDTAVVYCAR--RGYYMDVWGCTVTYVSS 157
DB 80 ADVSKGRFTISRDNKNTLYLQMSLRAPEDTAVVYCAKMSGVEFTDIMGGCTVTVSS 139
QY 158 GSGGS 162
DB 140 GSASA 144

RESULT 4
Q925S1 PRELIMINARY: PRT: 218 AA.
AC Q925S1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT Cloning of mouse genes related to repairing of intestinal epithelium

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ID	Q9UL90;	PRELIMINARY;	PRT;	113 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Mysin-reactive immunoglobulin heavy chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berner S.M.,			
RA	Young D.C.;			
RT	"Mysin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035024; AAD56260.1; -.			
DR	HSSP; P01772; 2FB4.			
DR	InterPro: IPR007110; Ig-Ilike.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig-V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PSS0835; IG-Like; 1.			
FT	NON_TER 1			
FT	NON_TER 1			
FT	NON_TER 113			
FT	NON_TER 113			
SEQUENCE	113 AA; 12437 MW; ED57FDD19086D07F CRC64;			

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Query Match      31.8%; Score 521.5; DB 4; Length 113;
Best Local Similarity 85.6%; Pred. No. 5.9e-32;
Matches 101; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

QY 40 QVQLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKLEWVAGIFPDGKNKYY 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVQLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKLEWVAFIRYDSNKKYY 60

QY 100 ADSVKGRFTISRDNKNTLYIQMNSLRADDTAVYVCARDRGYYMDVWGKGTIVTVSS 157
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 ADSVKGRFTISRDNKNTLYIQMNSLRADDTAVYVCARDKDLNT-----WGQGLTVTVSS 113

RESULT 8
Q96E61 PRELIMINARY; PRT; 236 AA.
ID 096E61
AC 096E61;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match      31.0%; Score 508; DB 4; Length 236;
Best Local Similarity 83.6%; Pred. No. 1.5e-30;
Matches 97; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 169 GGSQSGLVTPPSVSGAPGQRYTISCTGRSSNIGAGHDYHWYQQLPGTAPKLLIYDSDNR 228
   | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 16 GSAQSVTLAOPPSVSCAPGQTYTISCTGSTNGAGYAHWYQQFGAPAKVLLIYGNR 75

QY 229 PGVPDRFSGSKSGTSASLAIITGLQAEADADYYCQSYDSSLRGSVFGGTRKTVLG 284
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 76 PGVPDRFSGSKSGTSASLAIITGLQAEADADYYCQSYDSSLRGSVGAGTKTVLG 131

RESULT 9
Q9UL93 PRELIMINARY; PRT; 116 AA.
ID 09UL93
AC 09UL93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-9827139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP: P01772; 2F84.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match      30.8%; Score 504.5; DB 4; Length 116;
Best Local Similarity 84.6%; Pred. No. 1.1e-30;
Matches 99; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 41 VOLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKLEWVAGIFPDGKNKYYA 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 VOLVESGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKLEWVAVISYDGNKYYA 60

QY 101 DSVKGRFTISRDNKNTLYIQMNSLRADDTAVYVCARDRGYYMDVWGKGTIVTVSS 157
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 DSVKGRFTISRDNKNTLYIQMNSLRADDTAVYVCARDGAGG-IGLGYSGGLTVTVSS 116

RESULT 10
Q8WU38 PRELIMINARY; PRT; 573 AA.
ID 08WU38
AC 08WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match      30.6%; Score 502; DB 4; Length 573;
Best Local Similarity 42.4%; Pred. No. 1.2e-29;
Matches 131; Conservative 28; Mismatches 72; Indels 78; Gaps 12;

QY 40 QVQLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKLEWVAGIFPDGKNKYY 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKLEWVSGISWNSGSLCY 79

QY 100 ADSVKGRFTISRDNKNTLYIQMNSLRADDTAVYVCARDR-----GYVY-MDVWGKGTIV 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 ADSVKGRFTISRDNKNTLYIQMNSLRADDTALYYCAKGGSSYIGYYGMVWGKGTIV 139

QY 154 TVSSGGGGGGGGGGGSGVLTQPPSY-----PGQRYTISC--TGRSSNIGA 203
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 140 TVSSAP-----TKAPDVFTISGGRHPKDNQSPVYVLACLITGYHP---T 179

QY 204 GHDVHWY-----QQLPETAPKLLIYDDSDNRPSPGVPRFSGSKSGTASLAITGLQAEAD 259

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Db 180 SVTVWYMGTOFQPOFTEFIQORD-----SYMTSSQLS-TPLOQMRGE 224
QY 260 YVC--QSYDSSLRGSVF-----GGGKRYVYLGAAHHHHHNGA 296
Db 225 KCVVQVHRAKSKKEIFFWPESPKAQASSVPTAQAQAEGLAKATTAPATBTNTGCGGE 284
QY 297 EOKLISEED 305
Db 285 KKKEKEKEE 293

RESULT 11
QY509 PRELIMINARY: PRT; 147 AA.
AC QY509:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE VH3 Protein (Fragment).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig W.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -
DR HSSP: P01772; 2EB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match
Best Local Similarity 64.0%; Score 493; DB 4; Length 147;
Matches 103; Conservative 10; Mismatches 22; Indels 26; Gaps 4;

QY 40 QVOLVOSGGGVQPGKSLRLSCAASGFIFSSYGMHWVROAPGKGLEWAGIFYDGKNTY 99
Db 1 QVHLVESGGGVQPGKSLRLSCDASGFTSTYGMKSVROAPGKGLDVALISTDSTQY 60
QY 100 ADVKGRFTISRDNKNTLYLQMSLRADTAVYCCARD-----GYYY--MDVWGKGT 151
Db 61 ACSVKGRTYISRDNKNTLYLQMTSLRVEDTAVYCCAKNGYFDSYGYAGIDYWGQGT 120
QY 152 TTTVSSGGGGSGGGSGGSQSVLTQPPSVSG-APGQVY 191
Db 121 LVTVSSAS-----TKGVSVEPLAPSSKST 144

RESULT 12
Q9UL84 PRELIMINARY: PRT; 122 AA.
AC Q9UL84:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035030; AAD56266.1; -
DR HSSP: P01772; 2EB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match
Best Local Similarity 29.9%; Score 490; DB 4; Length 122;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 2;

QY 40 QVOLVOSGGGVQPGKSLRLSCAASGFIFSSYGMHWVROAPGKGLEWAGIFYDGKNTY 99
Db 1 EVQLVESGGGVQPGKSLRLSCAASFTSTYGMHWVROAPGKGLEWVAISNDGSKTY 60
QY 100 ADVKGRFTISRDNKNTLYLQMSLRADTAVYCCARD-RGY--YMDVWGKGTTVV 155
Db 61 ADVKGRFTYISRDNKNTLYLQMSLRADTAVYCCAKERGRRLVGTGYDYGQGLTVV 120
QY 156 SS 157
Db 121 SS 122

RESULT 13
Q8TC77 PRELIMINARY: PRT; 471 AA.
AC Q8TC77:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical Protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC024289; AAH24289.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7ACF588660E CRC64;

Query Match
Best Local Similarity 29.5%; Score 483; DB 4; Length 471;
Matches 97; Conservative 13; Mismatches 35; Indels 14; Gaps 2;

QY 40 QVOLVOSGGGVQPGKSLRLSCAASGFIFSSYGMHWVROAPGKGLEWAGIFYDGKNTY 99
Db 20 EVQLVESGGGLVKPGKSLRLSCAASGFTSTYGMHWVROAPGKGLEWVSMSSSYIY 79
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